PATENT APPLICATION

TELOMERASE REVERSE TRANSCRIPTASE TRANSCRIPTIONAL REGULATORY SEQUENCES AND METHODS OF USING

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TELOMERASE REVERSE TRANSCRIPTASE TRANSCRIPTIONAL REGULATORY SEQUENCES AND METHODS OF USING

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CROSS-REFERENCES TO RELATED APPLICATIONS

The present application is a continuation-in-part application ("CIP") of U.S. Patent Applications Serial No. ("USSN") 09/042,460 filed on March 16, 1998, which is a CIP of USSN 08/979,742, filed on November 26, 1997; and USSN

10   08/974,549, and USSN 08/974,584, both filed on November 19, 1997, and Patent Convention Treaty (PCT) International Application Serial No: PCT/US97/17618, for "Telomerase Reverse Transcriptase" (attorney docket No.:015389-002940PC) and PCT Application Serial No. PCT/US97/17885 for "Human Telomerase Catalytic Subunit" (attorney docket no. 015389-002600PC), both filed in the U.S. receiving office on

15   October 1, 1997, which are CIPs of USSN 08/915,503, filed August 14, 1997, USSN 08/912,951, filed August 14, 1997, and USSN 08/911,312, filed August 14, 1997; all three of which are CIPs of USSN 08/854,050, filed May 9, 1997, which is CIP of USSN 08/851,843, filed May 6, 1997, which is a CIP application of USSN 08/846,017, filed April 25, 1997, which is a CIP of USSN 08/844,419, filed April 18, 1997, which is a CIP

20   of USSN 08/724,643, filed on October 1, 1996. The afore-mentioned applications are explicitly incorporated herein by reference in their entirety and for all purposes.

STATEMENT AS TO RIGHTS TO INVENTIONS MADE UNDER FEDERALLY SPONSORED RESEARCH AND DEVELOPMENT

30   **FIELD OF THE INVENTION**

The present invention is related to novel nucleic acids comprising telomerase reverse transcriptase (TERT, or TRT) *cis*-acting transcriptional control

sequences. The present invention is further directed to methods of using these *cis*-acting transcriptional control sequences, for example, to drive heterologous gene sequences; to modulate the level of transcription of TERT or to isolate novel *trans*-acting regulatory factors which bind to and modulate the activity of a TERT promoter.

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BACKGROUND OF THE INVENTION

The following discussion is intended to introduce the field of the present invention to the reader. The citation of various references in this section is not to be construed as an admission of prior invention....

10   It has long been recognized that complete replication of the ends of eukaryotic chromosomes requires specialized cell components (Watson (1972) Nature New Biol. 239:197; Olovnikov (1973) J. Theor. Biol. 41:181). Replication of a linear DNA strand by conventional DNA polymerases requires an RNA primer, and can proceed only 5' to 3'. When the RNA primer bound at the extreme 5' ends of eukaryotic

15   chromosomal DNA strands is removed, a gap is introduced, leading to a progressive shortening of daughter strands with each round of replication. This shortening of telomeres, the protein-DNA structures physically located on the ends of chromosomes, is thought to account for the phenomenon of cellular senescence or aging of normal human somatic cells *in vitro* and *in vivo* (see, *e.g.*, Goldstein (1990) Science 249:1129; Martin

20   (1979) Lab. Invest. 23:86; Goldstein (1969) Proc. Natl. Acad. Sci. USA 64:155; Schneider (1976) Proc. Natl. Acad. Sci. USA, 73:3584; Harley (1990) Nature 345:458-460; Hastie (1990) Nature 346:866-868; Counter (1992) EMBO J. 11:1921-1929; Bodnar (1998) Science 279:349-52).

The length and integrity of telomeres is thus related to entry of a cell into a

25   senescent stage (*i.e.*, loss of proliferative capacity). Moreover, the ability of a cell to maintain (or increase) telomere length may allow a cell to escape senescence, *i.e.*, to become immortal.

The maintenance of telomeres is a function of a specific DNA polymerase known as telomerase reverse transcriptase (TERT, or TRT). Telomerase is a

30   ribonucleoprotein (RNP) that uses a portion of its RNA moiety as a template for telomere repeat DNA synthesis (see, *e.g.*, Morin (1997) Eur. J. Cancer 33:750). Consistent with the relationship of telomeres and TERT to the proliferative capacity of a cell (*i.e.*, the ability of the cell to divide indefinitely), telomerase activity is detected in immortal cell

lines and an extraordinarily diverse set of tumor tissues, but is not detected (*i.e.*, was absent or below the assay threshold) in normal somatic cell cultures or normal tissues adjacent to a tumor (see, U.S. Patent Nos. 5,629,154; 5,489,508; 5,648,215; and 5,639,613; see also, Morin (1989) Cell 59:521; Shay (1997) Eur. J. Cancer 33:787; Kim

5 (1994) Science 266:2011). Moreover, a correlation between the level of telomerase activity in a tumor and the likely clinical outcome of the patient has been reported (see *e.g.*, U.S. Patent No. 5,639,613; Langford (1997) Hum. Pathol. 28:416).

Telomerase activity has also been detected in human germ cells, proliferating stem or progenitor cells, and activated lymphocytes. In somatic stem or

10 progenitor cells, and in activated lymphocytes, telomerase activity is typically either very low or only transiently expressed (see, *e.g.*, Chiu (1996) Stem Cells 14:239; Bodnar (1996) Exp. Cell Res. 228:58; Taylor (1996) J. Invest. Dermatol. 106:759).

Accordingly, human TERT (hTERT, hTRT) is an ideal target for treating human diseases relating to cellular proliferation and senescence, such as cancer. The *cis*-

15 acting transcriptional control elements of TERT provided herein also allow for the identification of *trans*-acting transcription control factors. Moreover, the discovery and characterization of the TERT *cis*-acting sequences provide opportunities to develop useful disease therapies. The present invention fulfills this and other needs.

20 **SUMMARY OF THE INVENTION**

The invention provides an isolated, synthetic, or recombinant polynucleotide comprising a human telomerase reverse transcriptase (hTERT) promoter sequence. In alternative embodiments, the promoter sequence comprises at least 15, 50, 100, 150, 200, 250, 500, 1000, 2500 or at least 13,000 bases as set forth in residues 44 to

25 13490 in SEQ ID NO:1 or SEQ ID NO:2. Other embodiments include sequences starting within about one to 5 nucleotides of a translation start codon and ending at about 50, 100, 150, 200, 250, 500, 1000, 2500 or 13500 nucleotides upstream of the translation start codon in SEQ ID NO:1 or SEQ ID NO:2. The promoter sequence can comprise the sequence as set forth in residues 44 to 13490 in SEQ ID NO:1.

30 The invention provides an isolated, synthetic, or recombinant polynucleotide comprising a human telomerase reverse transcriptase (hTERT) promoter or a mouse telomerase reverse transcriptase (mTERT) sequence operably linked to a transcribable sequence. The transcribable sequence can encode a protein other than

hTERT or mTERT. The protein can be a cellular toxin. In one embodiment, the protein has activity that is not itself toxic to a cell, but which renders the cell sensitive to an otherwise nontoxic drug; *e.g.*, the protein can be a *Herpes* virus thymidine kinase. Alternatively, the transcribable sequence can encode a protein that is detectable by fluorescence, phosphorescence, or by virtue of its possessing an enzymatic activity. The detectable protein can be firefly luciferase, alpha-glucuronidase, alpha-galactosidase, chloramphenicol acetyl transferase, green fluorescent protein, enhanced green fluorescent protein, and the human secreted alkaline phosphatase.

The invention also provides a method for screening for a compound that binds to TERT promoter, such as an hTERT or an mTERT promoter, comprising the following steps: (i) providing an isolated, synthetic, or recombinant polynucleotide comprising a TERT promoter sequence and a test compound, (ii) contacting the polynucleotide with the test compound, and (iii) measuring the ability of the test compound to bind to the polynucleotide.

The invention also provides a method for a method for screening for a compound that modulates a TERT promoter, such as hTERT or mTERT promoter activity, comprising the following steps (i) providing a first polynucleotide comprising an isolated, synthetic, or recombinant TERT promoter sequence operably linked to a transcribable second nucleotide, and a test compound, (ii) contacting the polynucleotide with the test compound, and (iii) measuring the ability of the test compound to modulate transcription of the second nucleotide. The transcribable sequence can encode a protein. The protein can be detectable by fluorescence or phosphorescence or by virtue of its possessing an enzymatic activity. The detectable protein can be firefly luciferase, alpha-glucuronidase, alpha-galactosidase, chloramphenicol acetyl transferase, green fluorescent protein, enhanced green fluorescent protein, and the human secreted alkaline phosphatase.

The invention also provides a method for identifying a *cis*-acting transcriptional regulatory sequence that modulates a TERT promoter, such as hTERT or mTERT, promoter activity, comprising the following steps (i) providing a first construct comprising a first polynucleotide comprising an isolated, synthetic, or recombinant TERT promoter sequence operably linked to a transcribable second nucleotide, (ii) providing a second construct comprising a modification in a subsequence of the first polynucleotide of step 1 operably linked to a transcribable second nucleotide, and (iii) measuring independently under the same conditions the ability of the first construct and the second

construct to induce transcription of the transcribable second nucleotide, wherein an increase or decrease in the ability of the second modified construct to induce transcription of the transcribable second nucleotide as compared to the first unmodified construct identifies in the second modified construct a subsequence acting functionally as a *cis-*

5   acting transcriptional regulatory sequence that modulates TERT promoter activity.

The invention also provides a method for generating a cell that lacks a TERT promoter activity, comprising the following steps (i) providing a polynucleotide comprising an isolated, synthetic, or recombinant TERT promoter sequence; (ii) introducing into the cell the polynucleotide of step (i), and (iii) measuring ability of the

10   cell to transcribe TERT message; wherein the inability of the cell to transcribe TERT message indicates that a cell that lacks TERT promoter activity has been generated.   .

The invention also provides a genetically engineered cell lacking TERT, *e.g.,* hTERT or mTERT, promoter activity, produced by introducing into the cell a polynucleotide comprising an isolated, synthetic, or recombinant TERT promoter

15   sequence.

The invention also provides a composition comprising an isolated nucleic acid molecule comprising a TERT promoter, wherein the promoter comprises about 100 to about 200, 200 to about 400, 400 to about 900, or 900 to about 2500, or 2500 to about 5000 nucleotides upstream of a transcriptional start site in SEQ ID NO:1 or SEQ ID

20   NO:2.

The invention also provides a vector comprising a TERT promoter operably linked to a heterologous nucleic acid sequence, wherein the promoter comprises about 100 to about 200, 200 to about 400, 400 to about 900, or 900 to about 2500, or 2500 to about 5000 nucleotides upstream of a transcriptional start site in SEQ ID NO:1 or

25   SEQ ID NO:2.

The invention provides a transformed cell comprising a TERT promoter operably linked to a heterologous nucleic acid sequence, wherein the promoter comprises about 100 to about 200, 200 to about 400, 400 to about 900, or 900 to about 2500, or 2500 to about 5000 nucleotides upstream of a transcriptional start site in SEQ ID NO:1 or

30   SEQ ID NO:2. The heterologous nucleic acid can code for a cellular toxin. The cellular toxin can be a *Herpes* virus thymidine kinase, ricin, abrin, diphtheria, gelonin, *Pseudomonas* exotoxin A, tumor necrosis factor alpha (TNF-alpha), *Crotalus durissus*

terrificus toxin, *Crotalus adamenteus* toxin, *Naja naja* toxin, and *Naja mocambique* toxin.

The invention also provides a method of expressing a heterologous nucleic acid sequence in a cell comprising: (a) transforming said cell with a vector or an
5   expression cassette comprising a TERT promoter, wherein the promoter consists of about 100 to about 200, 200 to about 400, 400 to about 900, or 900 to about 2500, or 2500 to about 5000 nucleotides upstream of a transcriptional start site in SEQ ID NO:1 or SEQ ID NO:2, and wherein the promoter is operably linked to the heterologous nucleic acid sequence; and (b) growing said cell under conditions where the heterologous nucleic acid
10   sequence is expressed in said cell.

The invention also provides an isolated nucleic acid molecule which hybridizes to SEQ ID NO:1 or SEQ ID NO:2 under stringent hybridization conditions. The nucleic acid can consist of about 100 to about 200, 200 to about 400, 400 to about 900, or 900 to about 2500, or 2500 to about 5000 nucleotides upstream of a
15   transcriptional start site in SEQ ID NO:1 or SEQ ID NO:2. The stringent hybridization conditions can comprise a hybridization step comprising a salt concentration of about 0.02 molar at pH 7 and a temperature of about 60°C. The stringent hybridization conditions can also comprise a washing step at 65°C in 0.1X SSC, 0.1% SDS. In an alternative embodiment, the stringent hybridization conditions are selected to be about 5-
20   10°C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength and pH.

The invention also provides transgenic non-human animals comprising a TERT promoter sequence operably linked to transcribable sequence, such as a reporter gene. In a preferred embodiment, an hTERT promoter is operably linked to a reporter
25   gene in a transgenic mouse.

A further understanding of the nature and advantages of the present invention may be realized by reference to the remaining portions of the specification, the figures and claims.
30   All publications, GenBank deposited sequences, ATCC deposits, patents and patent applications cited herein are hereby expressly incorporated by reference for all purposes.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows a restriction map of lambda phage clone Gphi5, discussed in detail in Example 1, below.

Figure 2 shows the sequence of a Not1 fragment (SEQ ID NO:1) from the
5   lambda Gphi5 insert containing the hTERT promoter region.

Figure 3 shows the construction of an hTERT promoter-reporter plasmid, discussed in detail in Example 2, below.

Figure 4A shows, in the upper panel, sequence alignment of the murine and human TERT promoters. Also shown are·the positions of conserved cis-acting
10   transcriptional regulatory motifs, including the motifs designated as the "E-box" or "Myc/Max binding site" and SP1 sites. E-boxes are indicated by shaded ("shaded") sequence. SP1 sites are indicated by underlines. Figure 4A, lower panel, illustrates the proximal sequences of the 2.5 kb hTERT and E-box reporter constructs, including the · region deleted in the E-box reporter construct, as described below in Example 8. Figure
15   4B shows the alignment of human (residues -1106 to -1612) and mouse (residues -916 to -1340) TERT promoter sequences. Alignments were performed and identity calculated as described in Example 8. Cis-acting transcriptional regulatory elements common to both TERT promoters are indicated by shaded regions.

Figure 5 shows the sequence of the mouse telomerase reverse transcriptase
20   promoter sequence (SEQ ID NO:2).

DETAILED DESCRIPTION OF THE INVENTION

The invention provides novel isolated polynucleotides comprising cis-acting transcriptional control sequences of telomerase reverse transcriptase genes. The
25   polynucleotides of the invention include those based on or derived from genomic sequences of untranscribed, transcribed and intronic regions of TERT genes, including the human TERT (hTERT) and mouse TERT (mTERT) genes. Cis-acting TERT transcriptional control sequences, also referred to as the "TERT promoter sequences," include all cis-acting TERT transcriptional control elements and regulatory sequences,
30   including (without limitation) those that regulate and modulate timing and rates of transcription of the TERT gene. Thus, the TERT promoter sequences of the invention include cis-acting elements such as, *e.g.*, promoters, enhancers, transcription terminators, origins of replication, chromosomal integration sequences, introns, exons, and 5' and 3'

untranslated regions, with which proteins or other biomolecules interact to carry out and regulate transcription of the TERT transcript.

Isolating and Characterizing Human TERT Promoter Sequences

As described in Example 1, the hTERT promoter (SEQ ID NO:1) was obtained by sequencing an insert from a lambda phage isolated from a human genomic library. This lambda clone is designated "Gphi5" and has been deposited at the ATCC, with Accession No. 209024. Lambda Gphi5 contains a 15.3 kilobasepair (kbp) insert including approximately 13,500 bases 5' (upstream) to the hTERT coding sequence (*i.e.*, 5' untranscribed promoter sequence). These hTERT promoter sequences were further subcloned into plasmids. A Not1 fragment (SEQ ID NO:1) from lambda Gphi5 containing the hTERT promoter sequences was subcloned in opposite orientations into the Not1 site of pUC derived plasmids (designated pGRN142 and pGRN143, respectively, (see discussion below) and pGRN142 was sequenced.

In SEQ ID NO:1, the hTERT genomic insert begins at residue 44 and ends at residue 15375. The hTERT cDNA start site is at residue 13490. The hTERT ATG codon starts at residue 13545. Thus, untranscribed hTERT promoter sequences of the invention lie downstream of residue 44 and upstream of residue 13489 of SEQ ID NO:1. In immortal cells, a reporter gene driven by a sequence upstream of the TERT coding sequence drove expression as efficiently as the positive control (containing an SV40 early promoter and enhancer).

TERT promoter sequences (*i.e.*, TERT genomic sequences capable of driving transcription in a telomerase activity positive cell) of the invention also include intronic sequences.

Identification of Cis-Acting Transcriptional Regulatory Sequences in the Human and Mouse TERT Promoter

To identify cis-acting transcriptional regulatory sequences in human TERT (hTERT) and mouse TERT (mTERT) sequences 5' to their respective TERT coding sequence, the human and mouse promoter sequences were analyzed for sequence identity between themselves and publicly accessible sequences (see Example 8, below). Alignment of the first 300 bases upstream of the human and mouse coding sequences indicated a number of conserved regions, *i.e.* putative cis-acting transcriptional regulatory sequences (see Fig. 4A).

In particular, located at residues -34 to -29 upstream of the human TERT translation start site (ATG, A at 13545 of SEQ ID NO: 1) and at residues -32 to -27 upstream of the mouse TERT translation start site (ATG) are highly conserved motifs. They correspond to a cis-acting motif known to interact with c-Myc, the so-called "E-

5 box" or "Myc/Max binding site." Specifically, they are highly conserved with respect to the core nucleotides which comprise the E-box, nucleotides flanking the E-box and position of the E-box relative to the translation start site. A second E-box was identified at residues -242 to - 237 upstream of the human TERT translation start site. This second E-box was not conserved in the mouse promoter. These observations support the finding

10 (see discussion on E-box deletion construct experiments, below) that the conserved Myc binding site, by interacting with c-Myc as a *trans*-acting transcriptional regulatory factor, plays a major role in TERT promoter regulation and telomerase expression.

Sequence alignment identified additional conserved cis-acting transcriptional regulatory elements in the TERT gene promoter. For example, two SP1

15 binding sites, located at residue -168 to -159 and residue -133 to -121 relative to the TERT translation start site (Fig. 4A) were identified, which are highly conserved between the mouse and human TERT promoters.

Binding sites (*cis*-acting sequences) for a number of other transcription factors, including the sex determining region Y gene product (SRY), hepatic nuclear

20 factors 3-beta (HNF-3_) and 5 (HNF-5), TFIID-MBP, E2F and c-Myb were also found within this region of both the mouse and human promoters.

TERT-Specific Promoter Motif Identified

Further analysis of the human and mouse TERT promoter sequences indicated other regions of sequence conservation. In particular, a region with a high

25 degree of sequence identity between human and mouse promoter was found between residue -1106 and residue -1602 upstream of the human TERT translation start site and residue -916 and residue -1340 upstream of the mouse TERT translation start site (Fig. 4B). Thus, the invention provides *cis*-acting sequences specific for the modulation of TERT transcription.

30 In a preferred embodiment, the methods of the invention use these human and mouse TERT-specific transcriptional regulatory motifs to identify and isolate TERT-specific, and other, *trans*-acting transcriptional regulatory factors (as described in detail, below).

Screening and Isolating *Trans*-Acting TERT Transcriptional Modulators

The invention also provides the reagents and methods for screening and isolating *trans*-acting TERT transcriptional regulatory factors. Alternative embodiments include novel *in vitro* and cell-based *in vivo* assay systems to screen for TERT promoter

5   binding agents (*trans*-acting TERT transcriptional regulatory factors) using the nucleic acids of the invention.

Many assays are available that screen for nucleic acid binding proteins and all are adapted and used with the novel TERT sequences provided by the invention, as described below.

10   c-Myc Acts as a Potent Activator of TERT Gene Transcription

Use of recombinant constructs comprising TERT promoter sequences of the invention has, for the first time, demonstrated that c-Myc acts as a potent activator of telomerase activity by direct interaction with cis-acting regulatory sequences in the TERT promoter. c-Myc acts through the rapid upregulation of hTERT gene expression (see

15   Example 8, below). Significantly, the studies demonstrate that transcriptional activation of the hTERT promoter by c-Myc can be abrogated by deletion or mutation of a single cis-acting regulatory sequence, the "Myc/Max binding site," within the hTERT promoter. Furthermore, also as discussed below, the ability of an inducible c-Myc to enhance expression of hTERT is resistant to inhibition of protein synthesis.

20   Screening for Small Molecules and Biological Agents which are Modulators of the TERT Promoter

The invention also provides constructs, cell lines and methods for screening for small molecule modulators of TERT promoter activity *in vitro* and *in vivo*. Many assays are available that screen for small molecule modulators of TERT

25   transcription, including high throughput assays; all are adapted and used with the novel TERT sequences provided by the invention.

As described in detail in Example 5, below, various constructs containing hTERT promoter sequences driving a marker gene (in this example, the human secreted alkaline phosphatase, SEAP, gene) indicated that a fragment of approximately 2.5 kb of

30   hTERT promoter sequence contains sufficient sequence elements to support both activation and repression of gene expression in response to proliferation and/or growth arrest stimuli that control telomerase activity in a model cell line, IDH4. Clones were

selected and expanded for high throughput screening of small molecule activators of telomerase.

TERT Promoter used to Drive Heterologous Gene Sequences

The invention also provides constructs in which the TERT promoter

5   sequences of the invention are operably linked to a heterologous gene (in a preferred embodiment, a structural gene). In this way the heterologous gene is transcribed in the same cells at the same time the natural TERT transcript would be expressed. Thus, when the construct is expressed in a transformed cell or transgenic (non-human) animal, the heterologous gene (and protein, if the gene is a coding sequence) is expressed in the same

10   temporal pattern over the same cell range as the wild type, TERT promoter-driven TERT gene.

These constructs are useful for TERT promoter-based assays, for example, to identify biological modulators of TERT and telomerase activity. In alternative embodiments, the heterologous coding sequence operably linked to a TERT

15   promoter of the invention is a marker gene (*e.g.*, alkaline phosphatase, SEAP; ß-galactosidase), a modified TERT structural gene or a TERT antisense, a therapeutic gene (*e.g.*, a "cancer cell cytotoxic gene" as thymidine kinase).

In a further embodiment, cytopathic viruses are provided, in particular human cytopathic viruses, such as modified adenovirus or *Herpes* virus. Viruses, such as

20   adenovirus or *Herpes* virus require essential virally encoded genes to proliferate and lyse specific cells. If any one of these essential viral genes were modified such that expression of the essential element would be driven by the TERT promoter, proliferation of the virus, and its cytopathic effects, would be restricted to telomerase-expressing cells, in particular tumor cells.

25   **DEFINITIONS**

The following terms are defined infra to provide additional guidance to one of skill in the practice of the invention.

As used herein, the terms "allele" or "allelic sequence" refer to an alternative form of a nucleic acid sequence (*i.e.*, a nucleic acid corresponding to a TERT

30   promoter, particularly, an hTERT promoter). Alleles result from mutations (*i.e.*, changes in the nucleic acid sequence), and can produce differently regulated mRNAs. Common mutational changes that give rise to alleles are generally ascribed to natural deletions, additions, or substitutions of nucleotides. Each of these types of changes may occur

alone, in combination with the others, or one or more times within a given gene, chromosome or other cellular nucleic acid. Thus, the term "TERT promoter" includes allelic forms of TERT promoter sequences, *i.e.*, TERT cis-acting transcriptional control elements, including, *e.g.*, the exemplary human and mouse sequences described herein.

5   The term "amplifying" as used herein incorporates its common usage and refers to the use of any suitable amplification methodology for generating or detecting recombinant or naturally expressed nucleic acid, as described in detail, below. For example, the invention provides methods and reagents (*e.g.*, specific oligonucleotide PCR primer pairs) for amplifying (*e.g.*, by PCR) naturally expressed or recombinant nucleic

10   acids of the invention (*e.g.*, TERT promoter sequences of the invention) *in vivo* or *in vitro*. An indication that two polynucleotides are "substantially identical" can be obtained by amplifying one of the polynucleotides with a pair of oligonucleotide primers or pool of degenerate primers (*e.g.*, fragments of an TERT promoter sequence) and then using the · product as a probe under stringent hybridization conditions to isolate the second sequence

15   (*e.g.*, the TERT promoter sequence) from a genomic library or to identify the second sequence in, *e.g.*, a Northern or Southern blot.

          As used herein, the term "TERT promoter" includes any TERT genomic sequences capable of driving transcription in a telomerase activity positive cells. Thus, TERT promoters of the invention include without limitation cis-acting transcriptional

20   control elements and regulatory sequences that are involved in regulating or modulating the timing and/or rate of transcription of a TERT gene. For example, the TERT promoter of the invention comprises cis-acting transcriptional control elements, including enhancers, promoters, transcription terminators, origins of replication, chromosomal integration sequences, 5' and 3' untranslated regions, exons and introns, which are

25   involved in transcriptional regulation. These cis-acting sequences typically interact with proteins or other biomolecules to carry out (turn on/off, regulate, modulate, etc.) transcription.

          In alternative embodiments, the TERT promoter sequence comprises TERT sequences 5' (upstream) of the translational start site (ATG), for example, in one

30   embodiment, the hTERT promoter comprises residues 44 to 13545 of SEQ ID NO:1. Other embodiments include sequences starting within about one to 5 nucleotides of a translation start codon (for example in SEQ ID NO:1 or SEQ ID NO:2) and ending at about 50, 100, 150, 200, 250, 500, 1000, 2500 or 13500 nucleotides upstream of the

translation start codon. Such embodiments can optionally include other regulatory sequences, such as, exon and/or intron sequences. Another embodiment includes TERT intronic sequences with regulatory activity, as described in Example 2, below. hTERT promoters of the invention also include sequences substantially identical (as defined herein) to an exemplary hTERT promoter sequence of the invention, having the sequence set forth by SEQ ID NO:1. Similarly, mTERT promoters of the invention also include sequences substantially identical to an exemplary mTERT promoter sequence of the invention, having the sequence set forth by SEQ ID NO:2.

The term "heterologous" when used with reference to portions of a nucleic acid, indicates that the nucleic acid comprises two or more subsequences which are not found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences from unrelated genes arranged in a manner not found in nature; *e.g.*, a promoter sequence of the invention operably linked to a polypeptide coding sequence that, when operably linked, does not reform the naturally occuring TERT gene. For example, the invention provides recombinant constructs (expression cassettes, vectors, viruses, and the like) comprising various combinations of promoters of the invention, or subsequences thereof, and heterologous coding sequences, many examples of which are described in detail below.

As used herein, "isolated," when referring to a molecule or composition, such as, *e.g.*, an hTERT promoter sequence, means that the molecule or composition is separated from at least one other compound, such as a protein, DNA, RNA, or other contaminants with which it is associated *in vivo* or in its naturally occurring state. Thus, a nucleic acid sequence is considered isolated when it has been isolated from any other component with which it is naturally associated. An isolated composition can, however, also be substantially pure. An isolated composition can be in a homogeneous state. It can be in a dry or an aqueous solution. Purity and homogeneity can be determined, *e.g.*, using analytical chemistry techniques such as, *e.g.*, polyacrylamide gel electrophoresis (PAGE), agarose gel electrophoresis or high pressure liquid chromatography (HPLC).

As used herein, the terms "nucleic acid" and "polynucleotide" are used interchangeably, and include oligonucleotides (*i.e.*, short polynucleotides). They also refer to synthetic and/or non-naturally occurring nucleic acids (*i.e.*, comprising nucleic acid analogues or modified backbone residues or linkages). The terms also refer to deoxyribonucleotide or ribonucleotide oligonucleotides in either single-or double-

stranded form. The terms encompass nucleic acids containing known analogues of natural nucleotides. The term also encompasses nucleic acid-like structures with synthetic backbones. DNA backbone analogues provided by the invention include phosphodiester, phosphorothioate, phosphorodithioate, methyl-phosphonate, phosphoramidate, alkyl

5   phosphotriester, sulfamate, 3'-thioacetal, methylene (methylimino), 3'-N-carbamate, morpholino carbamate, and peptide nucleic acids (PNAs); see Oligonucleotides and Analogues, a Practical Approach, edited by F. Eckstein, IRL Press at Oxford University Press (1991); Antisense Strategies, Annals of the New York Academy of Sciences, Volume 600, Eds. Baserga and Denhardt (NYAS 1992); Milligan (1993) J. Med. Chem.

10   36:1923-1937; Antisense Research and Applications (1993, CRC Press). PNAs contain non-ionic backbones, such as N-(2-aminoethyl) glycine units. Phosphorothioate linkages are described in WO 97/03211; WO 96/39154; Mata (1997) Toxicol. Appl. Pharmacol. 144:189-197. Other synthetic backbones encompassed by the term include methyl-phosphonate linkages or alternating methylphosphonate and phosphodiester linkages

15   (Strauss-Soukup (1997) Biochemistry 36:8692-8698), and benzyl-phosphonate linkages (Samstag (1996) Antisense Nucleic Acid Drug Dev 6:153-156).

As used herein, the term "operably linked" refers to a functional relationship between two or more nucleic acid (e.g., DNA) segments. Typically, it refers to the functional relationship of a transcriptional regulatory sequence to a transcribed

20   sequence. For example, a TERT promoter sequence of the invention, including any combination of cis-acting transcriptional control elements, is operably linked to a coding sequence if it stimulates or modulates the transcription of the coding sequence in an appropriate host cell or other expression system. Generally, promoter transcriptional regulatory sequences that are operably linked to a transcribed sequence are physically

25   contiguous to the transcribed sequence, i.e., they are cis-acting. However, some transcriptional regulatory sequences, such as enhancers, need not be physically contiguous or located in close proximity to the coding sequences whose transcription they enhance.

As used herein, "recombinant" refers to a polynucleotide synthesized or

30   otherwise manipulated in vitro (e.g., "recombinant polynucleotide"), to methods of using recombinant polynucleotides to produce gene products in cells or other biological systems, or to a polypeptide ("recombinant protein") encoded by a recombinant polynucleotide. "Recombinant means" also encompass the ligation of nucleic acids

having coding or promoter sequences from different sources into an expression cassette or vector for expression of, *e.g.*, a fusion protein; or, inducible, constitutive expression of a protein (*i.e.*, a TERT promoter of the invention operably linked to a heterologous nucleotide, such as a polypeptide coding sequence).

5   As used herein, the "sequence" of a gene (unless specifically stated otherwise) or nucleic acid refers to the order of nucleotides in the polynucleotide, including either or both strands of a double-stranded DNA molecule, *e.g.*, the sequence of both the coding strand and its complement, or of a single-stranded nucleic acid molecule. For example, in alternative embodiments, the.promoter of the invention comprises

10   untranscribed, untranslated, and intronic TERT sequences, *e.g.*, as set forth in the exemplary SEQ ID NO:1 and SEQ ID NO:2.

          As used herein, the term "transcribable sequence" refers to any sequence which, when operably linked to a cis-acting transcriptional control element, *e.g.*, a promoter, such as the TERT promoters of the invention, and when placed in the

15   appropriate conditions, is capable of being transcribed to generate RNA, *e.g.*, messenger RNA (mRNA).

          The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of nucleotides (or amino acid residues)

20   that are the same, when compared and aligned for maximum correspondence over a comparison window, as measured using one of the following sequence comparison algorithms or by manual alignment and visual inspection. This definition also refers to the complement of a sequence. For example, in alternative embodiments, nucleic acids within the scope of the invention include those with a nucleotide sequence identity that is

25   at least about 60%, at least about 75-80%, about 90%, and about 95% of the exemplary TERT promoter sequence set forth in SEQ ID NO:1 (including residues 44 to 13544 of SEQ ID NO:1) or SEQ ID NO:2, and the intronic TERT sequences capable of driving a reporter gene in telomerase positive cells, as described below. Two sequences with these levels of identity are "substantially identical." Thus, if a sequence has the requisite

30   sequence identity to a TERT promoter sequence or subsequence of the invention, it also is a TERT promoter sequence within the scope of the invention. Preferably, the percent identity exists over a region of the sequence that is at least about 25 nucleotides in length, more preferably over a region that is at least about 50-100 nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are

5   designated. Default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated or default program parameters. A "comparison window", as used herein, includes reference to a segment of any one of the number of contiguous positions selected

10   from the group consisting of from 25 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, *e.g.*, by the local homology

15   algorithm of Smith & Waterman, Adv. Appl. Math. 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, J. Mol. Biol. 48:443 (1970), by the search for similarity method of Pearson & Lipman, Proc. Natl. Acad. Sci. USA 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575

20   Science Dr., Madison, WI), or by manual alignment and visual inspection (see, *e.g.*, Ausubel et al., supra).

One example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments to show relationship and percent sequence identity. It also plots a tree or

25   dendrogram showing the clustering relationships used to create the alignment. PILEUP uses a simplification of the progressive alignment method of Feng & Doolittle, J. Mol. Evol. 35:351-360 (1987). The method used is similar to the method described by Higgins & Sharp, CABIOS 5:151-153 (1989). The program can align up to 300 sequences, each of a maximum length of 5,000 nucleotides or amino acids. The multiple alignment

30   procedure begins with the pairwise alignment of the two most similar sequences, producing a cluster of two aligned sequences. This cluster is then aligned to the next most related sequence or cluster of aligned sequences. Two clusters of sequences are aligned by a simple extension of the pairwise alignment of two individual sequences. The

final alignment is achieved by a series of progressive, pairwise alignments. The program is run by designating specific sequences and their amino acid or nucleotide coordinates for regions of sequence comparison and by designating the program parameters. Using PILEUP, a reference sequence (*e.g.*, a TERT promoter sequence of the invention as set

5   forth by. *e.g.*, SEQ ID NO:1 or SEQ ID NO:2) is compared to another sequence to determine the percent sequence identity relationship (*i.e.*, that the second sequence is substantially identical and within the scope of the invention) using the following parameters: default gap weight (3.00), default gap length weight (0.10), and weighted end gaps. PILEUP can be obtained from the GCG sequence analysis software package, *e.g.*,

10   version 7.0 (Devereaux (1984) Nuc. Acids Res. 12:387-395).

Another example of algorithm that is suitable for determining percent sequence identity (*i.e.*, substantial similarity or identity) is the BLAST algorithm, which is described in Altschul (1990) J. Mol. Biol. 215:403-410. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology

15   Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul (1990) supra). These initial neighborhood

20   word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues, always < 0). For amino acid

25   sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X

30   determine the sensitivity and speed of the alignment. In one embodiment, to determine if a nucleic acid sequence is within the scope of the invention, the BLASTN program (for nucleotide sequences) is used incorporating as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=4, and a comparison of both strands. For amino acid

sequences, the BLASTP program uses as default parameters a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see, *e.g.*, Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915).

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, *e.g.*, Karlin (1993) Proc. Nat'l. Acad. Sci. USA 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (*e.g.*, total cellular or library DNA or RNA), wherein the particular nucleotide sequence is detected at least twice background, preferably 10 times background. In one embodiment, a nucleic acid can be determined to be within the scope of the invention (*e.g.*, is substantially identical to an hTERT promoter of the invention, as exemplified by residues 44 to 13544 of SEQ ID NO:1, or, SEQ ID NO:2, or, by an intronic promoter sequence, as described below) by its ability to hybridize under stringent conditions to another nucleic acid (such as the exemplary sequences described herein).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will primarily hybridize to its target subsequence, typically in a complex mixture of nucleic acid, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances, *e.g.*, depending on the length of the probe. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Probes, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent conditions are selected to be about 5-10°C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength and pH. The Tm is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium

(as the target sequences are present in excess, at Tm, 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes

5   (e.g., 10 to about 50 nucleotides) and at least about 60°C for long probes (e.g., greater than about 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal (e.g., identification of a nucleic acid of the invention) is about 5-10 times background hybridization. "Stringent" hybridization conditions that are used to identify

10   substantially identical nucleic acids within the scope of the invention include hybridization in a buffer comprising 50% formamide, 5x SSC, and 1% SDS at 42°C, or hybridization in a buffer comprising 5x SSC and 1% SDS at 65°C, both with a wash of 0.2x SSC and 0.1% SDS at 65°C, for long probes. For short probes, stringent hybridization conditions include hybridization in a buffer comprising 50% formamide,

15   5xSSC and 1% SDS at room temperature or hybridization in a buffer comprising 5 xSSC and 1% SDS at 37° C- 42°C, both with a wash of 0.2 x SSC and 0.1% SDS at 37° C-42°C. However, as is apparent to one of ordinary skill in the art, hybridization conditions can be modified depending on sequence composition. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M

20   NaCl, and 1% SDS at 37°C, and a wash in 1X SSC at 45°C. A positive hybridization is at least twice background. Those of ordinary skill will readily recognize that alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency.

GENERAL TECHNIQUES

25   The TERT promoter sequences of the invention and nucleic acids used to practice this invention, whether RNA, cDNA, genomic DNA, or hybrids thereof, may be isolated from a variety of sources, genetically engineered, amplified, and/or expressed recombinantly. Any recombinant expression system can be used, including, e.g., bacterial, yeast, insect or mammalian systems. Alternatively, these nucleic acids can be

30   chemically synthesized in vitro. Techniques for the manipulation of nucleic acids, such as, e.g., subcloning into expression vectors, labeling probes, sequencing, and hybridization are well described in the scientific and patent literature, see e.g., ed., MOLECULAR CLONING: A LABORATORY MANUAL (2ND ED.), Vols. 1-3, Cold

Spring Harbor Laboratory, (1989) ("Sambrook"); CURRENT PROTOCOLS IN
MOLECULAR BIOLOGY, Ausubel, ed. John Wiley & Sons, Inc., New York (1997)
("Ausubel"); LABORATORY TECHNIQUES IN BIOCHEMISTRY AND
MOLECULAR BIOLOGY: HYBRIDIZATION WITH NUCLEIC ACID PROBES, Part

5   I. Theory and Nucleic Acid Preparation, Tijssen, ed. Elsevier, N.Y. (1993) ("Tijssen").
Nucleic acids can be analyzed and quantified by any of a number of general means well
known to those of skill in the art. These include, *e.g.*, analytical biochemical methods
such as NMR, spectrophotometry, radiography, electrophoresis, capillary electrophoresis,
high pressure liquid chromatography (HPLC),.thin layer chromatography (TLC), and

10   hyperdiffusion chromatography, various immunological methods, such as fluid or gel
precipitin reactions, immunodiffusion (single or double), immunoelectrophoresis,
radioimmunoassays (RIAs), enzyme-linked immunosorbent assays (ELISAs), immuno-
fluorescent assays, Southern analysis, Northern analysis, dot-blot analysis, gel
electrophoresis (*e.g.*, SDS-PAGE), RT-PCR, quantitative PCR, other nucleic acid or

15   target or signal amplification methods, radiolabeling, scintillation counting, and affinity
chromatography.

Amplification of hTERT Promoter Sequences

The invention provides oligonucleotide primers that can amplify all or any
specific region within the TERT promoter sequence of the invention, including, *e.g.*,

20   specific promoter and enhancer subsequences. The nucleic acids of the invention can also
be generated or measured quantitatively using amplification techniques. Using the TERT
promoter sequences of the invention (*e.g.*, as in the exemplary hTERT SEQ ID NO:1 or
mTERT SEQ ID NO:2), the skilled artisan can select and design suitable oligonucleotide
amplification primers. Amplification methods are also well known in the art, and include,

25   *e.g.*, polymerase chain reaction, PCR (PCR PROTOCOLS, A GUIDE TO METHODS
AND APPLICATIONS, ed. Innis, Academic Press, N.Y. (1990) and PCR STRATEGIES
(1995), ed. Innis, Academic Press, Inc., N.Y., ligase chain reaction (LCR) (Wu (1989)
Genomics 4:560; Landegren (1988) Science 241:1077; Barringer (1990) Gene 89:117);
transcription amplification (Kwoh (1989) Proc. Natl. Acad. Sci. USA, 86:1173); and,

30   self-sustained sequence replication (Guatelli (1990) Proc. Natl. Acad. Sci. USA,
87:1874); Q Beta replicase amplification (Smith (1997) J. Clin. Microbiol. 35:1477-1491,
automated Q-beta replicase amplification assay; Burg (1996) Mol. Cell. Probes 10:257-
271) and other RNA polymerase mediated techniques (*e.g.*, NASBA, Cangene,

Mississauga, Ontario); see also Berger (1987) Methods Enzymol. 152:307-316,

Sambrook, Ausubel, Mullis (1987) U.S. Patent Nos. 4,683,195, and 4,683,202; Arnheim

(1990) C&EN 36-47; Lomell J. Clin. Chem., 35:1826 (1989); Van Brunt (1990)

Biotechnology, 8:291-294; Wu (1989) Gene 4:560; Sooknanan (1995) Biotechnology

5   13:563-564. Once amplified, TERT genomic DNA, TERT promoter sequences, and the

like, can be cloned, if desired, into any of a variety of vectors using routine molecular

biological methods; methods for cloning *in vitro* amplified nucleic acids are described,

e.g., in Wallace, U.S. Pat. No. 5,426,039.

Modified hTERT Promoter Sequences

10   The invention also provides for TERT promoter sequences that have been

modified in a site-specific manner to alter, add to, or delete some or all of the promoter's

functions. For example, specific base pairs can be modified to alter, increase or decrease

the binding affinity to trans-acting transcriptional regulatory factors, thus modifying the

relative level of transcriptional activation or repression. Modifications can also change

15   secondary structures of specific subsequences, such as those associated with many cis-

acting transcriptional elements. Site-specific mutations can be introduced into nucleic

acids by a variety of conventional techniques, well described in the scientific and patent

literature. Illustrative examples include, *e.g.*, site-directed mutagenesis by overlap

extension polymerase chain reaction (OE-PCR), as in Urban (1997) Nucleic Acids Res.

20   25:2227-2228; Ke (1997) Nucleic Acids Res 25:3371-3372, and Chattopadhyay (1997)

Biotechniques 22:1054-1056, describing PCR-based site-directed mutagenesis

"megaprimer" method; Bohnsack (1997) Mol. Biotechnol. 7:181-188; Ailenberg (1997)

Biotechniques 22:624-626, describing site-directed mutagenesis using a PCR-based

staggered re-annealing method without restriction enzymes; Nicolas (1997)

25   Biotechniques 22:430-434, site-directed mutagenesis using long primer-unique site

elimination and exonuclease III. See also Sambrook. and Ausubel. Modified TERT

promoter sequences of the invention can be further produced by chemical modification

methods, see, *e.g.*, Belousov (1997) Nucleic Acids Res. 25:3440-3444; Frenkel (1995)

Free Radic. Biol. Med. 19:373-380; Blommers (1994) Biochemistry 33:7886-7896.

30   Designing Antisense Oligonucleotides The invention also provides antisense

oligonucleotides capable of binding TERT promoter regions which, at least in part,

modulate TERT transcription and telomerase activity. For example, antisense

oligonucleotides that form triplexes with promoter regions inhibit the activity of that

promoter, see, *e.g.*, Joseph (1997) Nucleic Acids Res. 25:2182-2188; Alunni-Fabbroni

(1996) Biochemistry 35:16361-16369; Olivas (1996) Nucleic Acids Res 24:1758-1764.

Alternatively, antisense oligonucleotides that hybridize to the promoter sequence can be

used to inhibit promoter activity. Means to design antisense oligonucleotides are well

5   known in the art.

For example, antisense polynucleotides of the invention can comprise an

antisense sequence of at least 7 to 10 to about 20 or more nucleotides that specifically

hybridize to a sequence complementary to the TERT promoter sequences of the

invention (*e.g.*, including part of the exemplary hTERT SEQ ID NO:1 or mTERT SEQ

10   ID NO:2, as discussed above). Alternatively, the antisense polynucleotide of the

invention can be from about 10 to about 50 nucleotides in length or from about 14 to

about 35 nucleotides in length. In other embodiments, they are less than about 100

nucleotides or less than about 200 nucleotides. In general, the antisense polynucleotide

should be long enough to form a stable duplex (or triplex) but, if desired, short enough,

15   depending on the mode of delivery, to be administered *in vivo*. The minimum length of a

polynucleotide required for specific hybridization to a target sequence depends on several

factors, such as G/C content, positioning of mismatched bases (if any), degree of

uniqueness of the sequence as compared to the population of target polynucleotides, and

chemical nature of the nucleotides used in the antisense reagent (*e.g.*, methylphosphonate

20   backbone, peptide nucleic acid, phosphorothioate), among other factors. Methods

relating to antisense polynucleotides, are also described, *e.g.*, by ANTISENSE RNA

AND DNA, (1988), D.A. Melton, Ed., Cold Spring Harbor Laboratory, Cold Spring

Harbor, NY); Dagle (1991) Nucleic Acids Research 19:1805; Kim (1998) J. Controlled

Release 53:175-182; for antisense therapy, see, *e.g.*, Uhlmann (1990) Chem. Reviews

25   90:543-584; Poston (1998) J. Thorac. Cardiovasc. Surg. 116:386-396 (ex vivo gene

therapy); Haller (1998) Kidney Int. 53:1550-1558; Nguyen (1998) Cancer Res 58:5673-7.

Identifying hTERT Genomic Sequences

The present invention provides TERT promoters comprising genomic

sequences, including, *e.g.*, 5' (upstream) of an hTERT or mTERT transcriptional start site,

30   and intronic sequences, as described below. The promoter of the invention contains cis-

acting transcriptional regulatory elements involved in TERT message expression. It will

be apparent that, in addition to the nucleic acid sequences provided in hTERT SEQ ID

NO:1 or mTERT SEQ ID NO:2, additional TERT promoter sequences may be readily

obtained using routine molecular biological techniques. For example, additional hTERT genomic (and promoter) sequence may be obtained by screening a human genomic library using an hTERT nucleic acid probe having a sequence or subsequence as set forth in SEQ ID NO:1 (a nucleic acid sequence is within the scope of the invention if it hybridizes

5 under stringent conditions, as defined above, to an hTERT promoter sequence of the invention). Additional hTERT or mTERT genomic sequence can be readily identified by "chromosome walking" techniques, as described by, *e.g.*, Hauser (1998) Plant J 16:117-125; Min (1998) Biotechniques 24:398-400. Other useful methods for further characterization of TERT promoter sequences; *e.g.*, sequences flanking SEQ ID NO:1 or

10 mTERT SEQ ID NO:2, include those general methods described by, *e.g.*, Pang (1997) Biotechniques 22:1046-1048; Gobinda (1993) PCR Meth. Applic. 2:318; Triglia (1988) Nucleic Acids Res. 16:8186; Lagerstrom (1991) PCR Methods Applic. 1:111; Parker (1991) Nucleic Acids Res. 19:3055. As is apparent to one of ordinary skill in the art, these techniques can also be applied to any TERT promoter sequences in addition to the

15 human and mouse genomic sequences described herein.

Chemical Synthesis of TERT Promoter Sequences

The present invention also provides TERT polynucleotides that are produced by direct chemical synthesis. Chemical synthesis will typically be used to produce oligonucleotides and polynucleotides containing nonstandard nucleotides (*e.g.*,

20 probes, primers and antisense oligonucleotides) although nucleic acids containing only standard nucleotides can also be prepared. Direct chemical synthesis of nucleic acids can be accomplished by methods known in the art, such as, *e.g.*, the phosphotriester method of Narang (1979) Meth. Enzymol. 68:90; the phosphodiester method of Brown (1979) Meth. Enzymol. 68:109; the diethyl-phosphoramidite method of Beaucage (1981) Tetra.

25 Lett. 22:1859; and the solid support method of U.S. Patent No. 4,458,066. Chemical synthesis typically produces a single stranded oligonucleotide, which may be converted into double stranded DNA by hybridization with a complementary sequence, or by polymerization with a DNA polymerase and an oligonucleotide primer using the single strand as a template. One of skill will recognize that while chemical synthesis of DNA is

30 often limited to sequences of less than about 100 or 150 bases, longer sequences may be obtained by the ligation of shorter sequences or by more elaborate synthetic methods. It will be appreciated that the polynucleotides and oligonucleotides of the invention can be made using nonstandard bases (*e.g.*, other than adenine, cytidine, guanine, thymine, and

uridine) or nonstandard backbone structures to provide desirable properties (*e.g.*, increased nuclease-resistance, tighter binding, stability or a desired TM). Techniques for rendering oligonucleotides nuclease-resistant include those described in PCT publication WO 94/12633. A wide variety of useful modified oligonucleotides may be produced,

5 including oligonucleotides having a peptide nucleic acid (PNA) backbone (Nielsen (1991) Science 254:1497) or incorporating 2'-O-methyl ribonucleotides, phosphorothioate nucleotides, methyl phosphonate nucleotides, phosphotriester nucleotides, phosphorothioate nucleotides, and phosphoramidates. Still other useful oligonucleotides may contain alkyl and halogen-substituted sugar moieties comprising one of the

10 following at the 2' position: OH, SH, SCH_3, F, OCN, OCH_3OCH_3, $OCH_3O(CH_2)_nCH_3$, $O(CH_2)_nNH_2$ or $O(CH_2)_nCH_3$ where n is from 1 to about 10; C1 to C10 lower alkyl, substituted lower alkyl, alkaryl or aralkyl; Cl; Br; CN; CF_3; OCF_3; O-, S-, or N-alkyl; O-, S-, or N-alkenyl; $SOCH_3$; SO_2CH_3; ONO_2; NO_2; N_3; NH_2; heterocycloalkyl; heterocycloalkaryl; amino-alkylamino; polyalkylamino; substituted silyl; an RNA

15 cleaving group; a cholesteryl group; a folate group; a reporter group; an intercalator; a group for improving the pharmacokinetic properties of an oligonucleotide; or a group for improving the pharmacodynamic properties of an oligonucleotide and other substituents having similar properties. Folate, cholesterol or other groups which facilitate oligonucleotide uptake, such as lipid analogs, may be conjugated directly or via a linker at

20 the 2' position of any nucleoside or at the 3' or 5' position of the 3'-terminal or 5'-terminal nucleoside, respectively. One or more such conjugates may be used. Oligonucleotides may also have sugar mimetics such as cyclobutyls in place of the pentofuranosyl group. Other embodiments may include at least one modified base form or "universal base" such as inosine, or inclusion of other nonstandard bases such as queosine and wybutosine as

25 well as acetyl-, methyl-, thio- and similarly modified forms of adenine, cytidine, guanine, thymine, and uridine which are not as easily recognized by endogenous endonucleases. The invention further provides oligonucleotides having backbone analogues such as phosphodiester, phosphorothioate, phosphorodithioate, methylphosphonate, phosphoramidate, alkyl phosphotriester, sulfamate, 3'-thioacetal, methylene(methylimino), 3'-N-

30 carbamate, morpholino carbamate, chiral-methyl phosphonates, nucleotides with short chain alkyl or cycloalkyl intersugar linkages, short chain heteroatomic or heterocyclic intersugar ("backbone") linkages, or CH_2-NH-O-CH_2, CH_2-N(CH_3)-OCH_2, CH_2-O-N(CH_3)-CH_2, CH_2-N(CH_3)-N(CH_3)-CH_2 and O-N(CH_3)-CH_2-CH_2 backbones (where

phosphodiester is O-P-O-CH2), or mixtures of the same. Also useful are oligonucleotides having morpholino backbone structures (see. *e.g.*, U.S. Patent No. 5,034,506).

IDENTIFYING TERT PROMOTER SUBSEQUENCES BOUND BY *TRANS-* ACTING TRANSCRIPTIONAL REGULATORY FACTORS

5   The invention provides means to identify and isolate trans-acting transcriptional regulatory factors that are involved in modulating the activity of the TERT promoter. Identification of cis-acting motifs by, *e.g.*, sequence identity comparison, as discussed above, can be a useful initial means to identify promoter sequences bound by trans-acting factors. For example, as discussed above, the hTERT and mTERT promoters

10   contain a variety of cis-acting motifs. The hTERT promoter contains the motif known to bind to c-Myc (the "E-box" or "Myc/Max binding site"). Two SP1 binding sites are located starting at residue -168 and starting at residue -134 (Fig. 3A). Other identified motifs include the sex determining region Y gene product (SRY), hepatic nuclear factors 3-beta (HNF-3_) and 5 (HNF-5), TFIID-MBP, E2F and c-Myb cis-acting transcriptional

15   regulatory elements. All other cis-acting transcriptional regulatory elements known in the art (searchable by, *e.g.*, public data base, *e.g.*, http://www.ncbi.nlm.nih.gov/PubMedl) present in the TERT promoter sequences described herein are incorporated by the invention. To identify these motifs, a variety of comparison algorithms can be used. See, *e.g.*, Karas (1996) Comput. Appl. Biosci. 12:441-6; Frech (1997) Pac Symp Biocomput.

20   7:151-62; Brzma (1998) Genome Res 8:1202-1215; Tsunoda (1998) Pac Symp Biocomput :1998:252-63.

In addition to sequence identity analysis, TERT cis-acting transcriptional regulatory elements can be identified or confirmed by any means known in the art, including, *e.g.*, promoter activity assays, DNase assays, binding assays (*e.g.*, mobility

25   shift assays), oligonucleotide affinity column chromatography, and the like.

After positive or tentative identification of a cis-acting binding site in a TERT promoter, these sequences are used to isolate the trans-acting transcriptional regulatory factor(s) by any means known in the art. In a preferred embodiment, the trans-acting factors are isolated using sequence-specific oligonucleotide affinity

30   chromatography, the oligonucleotides comprising TERT sequences of the invention.

Another embodiemtn for identifying transcriptional regulatory motifs involves modifying putative cis-acting regulatory subsequences and assessing the change, if any, of the resultant TERT promoter to modulate transcription. The modification can

be, *e.g.*, one or more residue deletions, residue substitution(s), chemical alteration(s) of nucleotides, and the like. The (modified) promoter can be operably linked to TERT, or any transcribable sequence (*e.g.*, "reporter genes"). The relative increase or decrease the modification has on transcriptional rates can be determined, *e.g.*, by measuring the ability

5   of the unaltered TERT promoter to transcriptionally activate the reporter coding sequence under the same conditions as used to test the modified promoter. An increase or decrease in the ability of the modified TERT promoter to induce transcription as compared to the unmodified promoter construct identifies a cis-acting transcriptional regulatory sequence that is involved in the modulation of TERT promoter activity.

10   The reporter gene can encode any detectable protein known in the art, *e.g.*, detectable by fluorescence or phosphorescence or by virtue of its possessing an enzymatic activity. In alternative embodiments, the detectable protein is firefly luciferase, alpha-glucuronidase, alpha-galactosidase, chloramphenicol acetyl transferase, green fluorescent protein, enhanced green fluorescent protein, and the human secreted alkaline phosphatase.

15   Another embodiment tests the ability of these cis-acting elements to bind soluble polypeptide trans-acting factors isolated from different cellular compartments, particularly trans-acting factors expressed in nuclei. For identification and isolation of factors that stimulate transcription, cell (*e.g.* nuclear) extracts from cells that express TERT are used. Means to conduct these studies are well known in the art.

20   Furthermore, as discussed further below, once a cis-acting motif, or element, is identified, it can be used to identify and isolate trans-acting factors in a variety of cells and under different conditions (*e.g.*, cell proliferation versus cell senescence). Accordingly, the invention provides a method for screening for trans-acting factors that modulate TERT promoter activity under a variety of conditions, developmental states,

25   and cell types (including, *e.g.*, normal versus immortal versus malignant phenotypes).

The cis-acting transcriptional regulatory sequences of the invention that modulate TERT promoter activity can also be used as oligonucleotides which, upon introduction into a cell, can bind trans-acting regulatory factors to modulate TERT transcription *in vivo*. This results in increased or decreased cell proliferative capacity for

30   the treatment of various diseases and conditions, as discussed below.

HIGH THROUGHPUT SCREENING OF SMALL MOLECULE MODULATORS OF TERT TRANSCRIPTION

The invention provides constructs and methods for screening modulators, in a preferred embodiment, small molecule modulators, of TERT promoter activity *in*

5 *vitro* and *in vivo*. The invention incorporates all assays available to screen for small molecule modulators of TERT transcription. In a preferred embodiment, high throughput assays are adapted and used with the novel TERT promoter sequences and constructs provided by the invention, *e.g.*, the hTERT and mTERT promoter sequences described herein. See, *e.g.*, Schultz (1998) Bioorg Med Chem Lett 8:2409-2414; Weller (1997) Mol

10 Divers. 3:61-70; Fernandes (1998) Curr Opin Chem Biol 2:597-603; Sittampalam (1997) Curr Opin Chem Biol 1:384-91.

In alternative embodiments, recombinant constructs contain hTERT promoter sequences driving a marker, such as an alkaline phosphatase marker gene (SEAP) or a §-galactosidase gene. Using a SEAP expressing construct of the invention, it

15 was demonstrated that a TERT promoter fragment of approximately 2.5 kb is sufficient to activate and repress TERT transcription in response to proliferation and/or growth arrest stimuli in a model cell line, IDH4. Two cell clones, ID245-1 and ID245-16 whose SEAP profiles closely matched telomerase activity after TERT upregulation by dexamethasone were selected and expanded for high throughput screening of small molecule activators of

20 telomerase.

TREATMENT OF TELOMERASE-RELATED DISEASES

The present invention provides TERT promoter sequences useful for the treatment of diseases and disease conditions. The recombinant and synthetic nucleic acids comprising TERT promoter, or TERT antisense complementary sequences, can be

25 used to create or elevate telomerase activity in a cell, as well as to inhibit telomerase activity in cells in which it is not desired. In a preferred embodiment, human TERT promoter sequences or antisense sequences are used for the treatment of human diseases and disease conditions.

Identification of cis-acting transcriptional regulatory sequences by the

30 invention further provides for the design of targeted sequences that, as oligonucleotides, can modify TERT promoter activity. In one embodiment, telomerase activity is created or elevated by binding significant amounts of a trans-acting transcriptional repressor or down-regulator with a nucleic acid that binds specifically to the repressor. In another

embodiment, telomerase activity is down-regulated by antisense oligonucleotides binding to promoter sequences (see discussion, above). Similarly, telomerase activity can be inhibited by binding significant amounts of a trans-acting transcriptional activator or up-regulator with a nucleic acid that binds specifically to the activator; or telomerase activity

5   is up-regulated by antisense oligonucleotides binding to promoter sequences involved in telomerase repression. Thus, inhibiting, activating or otherwise altering a telomerase activity (*e.g.*, telomerase catalytic activity, fidelity, processivity, telomere binding, etc.) in a cell can be used to change the proliferative capacity of the cell.

For example, reduction of telomerase activity in an immortal cell, such as

10   a malignant tumor cell, can render the cell mortal. Conversely, increasing the telomerase activity in a cell line or a mortal cell (*e.g.*, most human somatic cells) can increase the proliferative capacity of the cell. For example, expression of hTERT protein in dermal fibroblasts, thereby increasing telomere length, will result in increased fibroblast proliferative capacity. Such expression can slow or reverse age-related degenerative

15   processes, such as, *e.g.*, the age-dependent slowing of wound closure (see, *e.g.*, West (1994) Arch. Derm. 130:87). Thus, in one aspect, the present invention provides reagents and methods useful for treating diseases and conditions characterized by the presence, absence, or altered amount of human telomerase activity in a cell (where the diseases and conditions are susceptible to treatment using the compositions and methods disclosed

20   herein). These diseases include, *e.g.* cancers, other diseases of cell proliferation (particularly, degenerative and aging processes and diseases of aging), immunological disorders, infertility (or fertility).

Treatment of Cancer

The present invention provides methods and compositions for reducing

25   TERT promoter activity (and hence telomerase activity) in immortal cells and tumor cells for treating cancer. Cancer cells (*e.g.*, malignant tumor cells) that express telomerase activity (telomerase-positive cells) can be mortalized by decreasing or inhibiting TERT promoter activity. Moreover, because measurable telomerase activity levels correlate with disease characteristics such as metastatic potential (see, *e.g.*, U.S. Patent Nos.

30   5,639,613; 5,648,215; 5,489,508; and Pandita (1996) Proc. Am. Ass. Cancer Res. 37:559), any reduction in TERT promoter activity could reduce the aggressive nature of a cancer to a more manageable disease state. As noted above, immortal cells and cancer

cells, as opposed to non-cancerous, mortal cells, have high levels of TERT promoter activity.

Taking advantage of this characteristic, in one embodiment of the invention, a TERT promoter sequence is operably linked to a gene encoding a toxin and introduced into a cell to kill the cell (a number of protein toxins are well known in the art including, *e.g.*, ricin, diphtheria, gelonin, Pseudomonas toxin, abrin). If or when TERT transcriptional activators are expressed or activated in the cell, the toxin will be expressed, resulting in specific cell killing.

Alternatively, the TERT promoter-linked gene can encode a protein having activity that is not itself toxic to a cell, but which renders the cell sensitive to an otherwise nontoxic drug (such as, *e.g.*, Herpes virus thymidine kinase).

In another embodiment, the invention takes advantage of the fact that normal cytopathic viruses, in particular human cytopathic viruses, such as adenovirus or Herpes virus, require essential virally encoded genes to proliferate thereby lysing specific cells. If any one of these essential viral genes was modified such that expression of the essential element was driven by the TERT promoter, proliferation of the virus and its cytopathic effects would be restricted to tumor cells and other telomerase expressing cells. Accordingly, the invention provides constructs and methods for killing telomerase positive cells (*e.g.*, cancer cells, germ cells) wherein TERT promoter sequences of the invention are operably linked to such viral "essential element" genes. For use in human cells, human cytopathic viruses modified with hTERT promoter sequences are preferred. Any one or more of the genes required for the replication and packaging of the virus could be modified to be driven by the TERT promoter. For instance, in one embodiment, expression of the E1a gene of adenovirus, which is required for the activation of expression of a cascade of adenoviral genes, is placed under the control of the hTERT promoter.

Thus, expression of E1a, and hence downstream replication of the virus, occurs only in those cells that express telomerase (*i.e.*, tumor cells). Likewise, a recombinant adenovirus of the invention is designed so the adenoviral capsid genes are under the control of a TERT promoter. While this construct replicates its DNA in most cell types, it packages itself into active, infectious (and cytotoxic) virus only in those cells that express telomerase. Thus, when these constructs are used as cancer therapeutics, the conditionally replicative virus only infects and yields a productive infection in tumor cells

(with no effect in "normal" cells that do not express telomerase). Infection of normal cells that do not express telomerase is expected to produce either no or abortive production of the virus, depending on which gene is driven by the TERT promoter. Thus, these recombinant viruses of the invention allow the natural, yet tumor specific,

5 amplification of an oncolytic virus.

In alternative embodiments, many other elements are incorporated into such an TERT promoter restricted oncolytic virus or a TERT promoter restricted replicative but not lytic. Genes encoding suicide genes, marker genes, apoptotic genes or cell cycle regulators are incorporated in the TERT promoter restricted conditionally

10 replicative recombinant virus. Expression of these elements in such a virus would assist the arrest of tumor growth. In one embodiment, elements to be included within these conditionally replicative viruses of the invention are structures that inhibit telomerase activity. These telomerase inhibitors could incorporate inhibitory oligonucleotides, dominant-negative inhibitors of TERT, or the gene for any agent that would disrupt or

15 prevent TR/TERT assembly, interactions, or activity.

Other elements can also be included in the "TERT promoter restricted" vectors of the invention (*i.e.*, vectors expressing TERT promoter driven genes which are only expressed in telomerase-positive cells). For example, small inhibitory RNA molecules, preferably targeting cancer cells, such as RNA targeting telomerase activity

20 can be synthesized *in vivo* using a recombinant adenovirus vector. Exemplary sequences are provided in USPN 5,858,777 and GB 20890.4. RNA production from the adenovirus can be achieved by a variety of expression cassettes. For cell growth inhibition purposes, RNA polymerase III expression cassettes based on the structure of tRNA genes and other RNA polymerase III transcripts, including the U6 snRNA gene, as well as RNA

25 polymerase II snRNP (U1, U2) transcripts are preferred due to their ability to produce high levels of transcripts.

The hTERT promoter restricted viruses of the invention can be designed to express inhibitory RNAs, as antisense molecules complementary to several regions of the hTR molecule, including the template region. The inhibitory RNAs can also mimic

30 sequences and/or structures present in the RNA component of telomerase (*e.g.*, hTR), including potential binding site(s) for TERT or other telomerase-associated proteins that might interact with the RNA component. Other elements can also be designed to

generate inhibitory RNAs to target TERT mRNA by preventing its normal processing, folding, modification, transport and/or translation.

Other cytopathic viral vectors of the invention can be designed to generate RNA molecules with sequences necessary for cytoplasmic export and translation into peptides. The resulting polypeptides or peptides can be designed to target telomerase components or other molecules that are associated with telomerase thereby influencing telomerase catalytic activity. The peptides that inhibit telomerase will be produced at high level, paralleling the amount of RNA. For example, peptides could be designed to mimic the stretch of amino acids in hTERT involved in its binding to hTR, thereby acting as competitors in the assembly of a functional telomerase.

The TERT promoter restricted viral vectors of the invention can also be designed to generate peptides or polypeptides for any domain of TERT involved in interactions with other proteins and disrupt contacts that are essential for telomerase function. Other TERT promoter restricted viruses of the invention can be designed to generate polypeptides to bind to telomere complexes and prevent access and/or docking of telomerase or to generate immunogenic peptides, in part TERT peptides.

Other TERT promoter restricted viral vectors of the invention can be designed to generate polypeptides to mimic a variety of apoptosis inducing agents observed during programmed cell death and could result in the onset of apoptosis.

TERT promoter restricted viruses do not necessarily need to be cytopathic. The TERT promoter conditionally restricted virus could be used to amplify any sequences or any element in any TERT expressing cell, *e.g.*, a tumor cell.

Any of these embodiments can be provided with the conditionally replicative viruses of the invention. The TERT promoter constructs of the invention can also be used in gene therapy vectors to prevent telomerase activation and result in specific "mortalization" or death of telomerase-positive cells. Similarly, these gene therapy methods may be used for "treating" a genetic predilection for cancers.

Treatment of other Conditions

The present invention also provides compositions and methods useful for treatment of diseases and disease conditions (in addition to cancers) characterized by under- or over-expression of telomerase or TERT gene products. Examples include, *e.g.*, diseases of cell proliferation, diseases resulting from cell senescence (particularly processes and diseases of aging), immunological disorders, infertility, and diseases of

immune dysfunction. Certain diseases of aging are characterized by cell senescence-associated changes due to reduced telomere length (compared to younger cells), resulting from the absence (or much lower levels) of telomerase activity in the cell. Decreased telomere length and decreased replicative capacity contribute to these diseases.

5   Telomerase activity (resulting in increased telomere length) can be upregulated by, *e.g.*, increasing TERT promoter activity in the cell.

The present invention, by providing methods and compositions for modulating TERT promoter activity, also provides methods to treat infertility. Human germline cells (*e.g.*, spermatogonia cells, their-progenitors or descendants) are capable of

10   indefinite proliferation and characterized by high telomerase activity. Abnormal or diminished levels of TERT gene products can result, *e.g.*, in inadequate or abnormal production of spermatozoa, leading to infertility or disorders of reproduction. Accordingly, "telomerase-based" infertility can be treated using the methods and compositions described herein to increase TERT promoter activity levels. Similarly,

15   because inhibition of telomerase may negatively impact spermatogenesis, oogenesis, and sperm and egg viability, the compositions of the invention capable of inhibiting hTERT promoter activity can have contraceptive effects when used to reduce hTERT levels in germline cells.

In a further embodiment, the invention provides methods and composition

20   useful for decreasing the proliferative potential of telomerase-positive cells such as activated lymphocytes and hematopoietic stem cells by reducing TERT promoter activity. Thus, the invention provides means for effecting immunosuppression. Conversely, the methods and reagents of the invention are useful in immunostimulation by increasing TERT promoter activity (resulting in increased proliferative potential) in immune cells,

25   including hematopoietic stem cells (that express a low level of telomerase or no telomerase prior to therapeutic intervention).

MODULATING TERT PROMOTER ACTIVITY

As is clear from the foregoing discussion, modulation of the level of TERT promoter transcriptional activity (and thus, the levels of telomerase or telomerase activity

30   of a cell) can have a profound effect on the proliferative potential of the cell, and so has great utility in treatment of disease. This modulation can either be a decrease or an increase in TERT promoter activity. The promoter activity-modulatory nucleic acid

molecules of the invention can act through a number of mechanisms. However, the invention is not limited to any particular mechanism of action.

For example, TERT promoter activity may be decreased or increased by single stranded antisense sequences that directly bind to TERT promoter sequences. This will result in decrease in affinity or inhibition of trans-acting transcriptional regulatory factors binding to critical TERT promoter sequences (*e.g.*, TATA boxes, CAAT boxes, and the like). When the cis-acting element bound by a trans-acting factor has inhibitory activity, the binding of the oligonucleotide would result in upregulation of TERT transcription. Conversely, if the promoter subsequence, when bound by a trans-acting factor, has upregulating activity, the binding of the oligonucleotide would result in down-regulation of TERT transcription. In another embodiment, double-stranded oligonucleotides representing TERT promoter subsequences directly bind trans-acting transcriptional modulatory elements, thus preventing them from binding their corresponding cis-acting elements. In summary, TERT promoter activity may be increased or decreased through any of several mechanisms, or a combination of mechanisms. These include any means apparent to those of skill upon review of this disclosure.

Antisense Oligonucleotides Binding to TERT Promoter Control Sequences

As discussed above, antisense oligonucleotides which hybridize to TERT promoter sequences will inhibit the binding of trans-acting transcriptional upregulatory agents to critical TERT promoter sequences. Furthermore, the result will be activation or repression of TERT transcriptional activity, depending on whether the promoter subsequence is down-regulatory or up-regulatory, respectively. Thus, the invention provides antisense oligonucleotides directed to the TERT promoter (cis-acting) binding sites for c-Myc (the "E-box" or "Myc/Max binding sites"), SP1, Y gene product (SRY), hepatic nuclear factors 3-beta (HNF-3_), 5 (HNF-5), TFIID-MBP, E2F, c-Myb, TATA boxes, CAAT boxes, and other, as described herein.

While the invention is not limited by any particular mechanism, oligonucleotides of the invention can also bind to double-stranded or duplex TERT promoter sequences. They can bind in a folded region, forming a triple helix, or "triplex" nucleic acid. Triple helix formation results in inhibition of TERT promoter activity by, *e.g.*, disrupting the secondary structure of the promoter sequence, resulting in a new conformation which the trans-acting factor cannot bind with sufficient affinity to have a

transcriptional-modifying effect. Alternatively, triple helix formation (induced by the binding of the antisense oligonucleotide of the invention) compromises the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or regulatory trans-acting molecules to occur. Triplex oligo- and polynucleotides design

5   construction (also discussed, above) is well described in the art; see, *e.g.*, Cheng (1988) J. Biol. Chem. 263:15110; Ferrin (1991) Science 354:1494; Ramdas (1989) J. Biol. Chem. 264:17395; Strobel (1991) Science 254:1639; Rigas (1986) Proc. Natl. Acad. Sci. U.S.A. 83: 9591) Carr, 1994, MOLECULAR AND IMMUNOLOGIC APPROACHES, Futura Publishing Co, Mt Kisco NY; Rininsland (1997) Proc.

10   Natl. Acad. Sci. USA 94:5854; Perkins (1998) Biochemistry 37:11315-11322.

Double-Stranded Oligonucleotides Bind to Trans-Acting Molecules

The cis-acting transcriptional regulatory sequences of the invention can also be used as oligonucleotides which, upon introduction into a cell, can bind trans-acting regulatory factors to modulate TERT transcription *in vivo*. These oligonucleotides

15   can be delivered to target cells through an appropriate delivery scheme or they can be synthesized *in vivo* by recombinant expression systems (vectors, viruses, and the like). Appropriate expression systems, delivery mechanisms, formulations, and the like are well known in the art (discussed in more detail, below).

ADMINISTRATION OF OLIGONUCLEOTIDES *IN VIVO*

20   The therapeutic nucleic acids and methods of the invention involve the administration of oligonucleotides or polynucleotides that function to inhibit or stimulate TERT promoter activity under *in vivo* physiological conditions. In one embodiment, these nucleic acids are, *e.g.*, single stranded antisense sequences capable of binding to promoter sequences. In an alternative embodiment, they are double stranded nucleic

25   acids capable of binding trans-acting transcriptional regulatory factors. They should be sufficiently stable under physiological conditions for a period of time to obtain a therapeutic effect. As noted above, modified nucleic acids may be useful in imparting such stability, as well as for targeting delivery of the oligonucleotide to the desired tissue, organ, or cell. Oligo- and poly-nucleotides can be delivered directly as a drug in a

30   suitable pharmaceutical formulation, or indirectly by means of introducing a nucleic acid expression system (*e.g.*, cassette, vector) which can recombinantly generate the hTERT promoter modulating oligonucleotides into a cell, *e.g.*, by "gene therapy" (see below).

Oligonucleotides or expression vectors can be administered by any means known in the art, including, *e.g.*, liposomes, immunoliposomes, ballistics, direct uptake into cells, and the like. For treatment of disease (see discussion above), the oligonucleotides of the invention will be administered to a patient in a therapeutically

5 effective amount. A therapeutically effective amount is an amount sufficient to ameliorate the symptoms of the disease or modulate hTERT promoter activity (thereby affecting telomerase activity) in the target cell. Methods useful for delivery of oligonucleotides for therapeutic purposes are well known in the art and are described, *e.g.*, in U.S. Patent 5,272,065.

10 Telomerase activity can be measured by a variety of means, *e.g.*, by TRAP assay or other suitable assay of telomerase biological function, as discussed in detail in related applications.

GENE THERAPY

The invention provides methods and reagents for affecting TERT promoter

15 activity *in vivo* by gene therapy. In one embodiment, as discussed above, gene therapy is used to deliver oligonucleotides that modulate TERT promoter activity by directly binding to cis-acting sequences or, alternatively, that bind to trans-acting regulatory factors. One embodiment exploits the fact that the TERT promoter is only relatively active in a very limited range of cell types, including, significantly, cancer cells.

20 **TERT Promoter Operably Linked to Cellular Toxins**

In one embodiment, the TERT promoter of the invention is operably linked to a transcribable sequence which encodes a cellular toxin. A number of polypeptide toxins that can be recombinantly generated are well known in the art including, *e.g.*, ricin, abrin (Hughes (1996) Hum. Exp. Toxicol. 15:443-451), diphtheria,

25 gelonin (Rosenblum (1996) Cancer Immunol. Immunother. 42:115-121), *Pseudomonas* exotoxin A, tumor necrosis factor alpha (TNF-alpha), *Crotalus durissus terrificus* toxin, *Crotalus adamenteus* toxin, *Naja naja* toxin, and *Naja mocambique* toxin, see, *e.g.*, Rodriguez (1998) Prostate 34:259-269; Mauceri (1996) Cancer Res. 56:4311-4314.

The cellular toxin can also be capable of inducing apoptosis, such as, *e.g.*,

30 a direct inducer of apoptosis, such as the ICE-family of cysteine proteases, the Bcl-2 family of proteins, bax, bclXs and caspases, see, *e.g.*, Favrot (1998) Gene Ther. 5:728-739; McGill (1997) Front. Biosci. 2:D353-D379; McDonnell (1995) Semin. Cancer Biol. 6:53-60.

Alternatively, the sequence under the control of the TERT promoter can code for polypeptides having activity that is not itself toxic to a cell, but which renders the cell sensitive to an otherwise nontoxic drug, *e.g.*, Herpes virus thymidine kinase (GSV-TK). The HSV-TK is innocuous but converts the anti-herpetic agent ganciclovir

5 (GCV) to a toxic product that interferes with DNA replication in proliferating cells (see, *e.g.*, Delaney (1996) J. Neurosci. 16:6908-6918; Heyman (1989) Proc. Natl. Acad. Sci. USA 86:2698-2702). The art describes numerous other suitable toxic or potentially toxic proteins and systems that may be applied in this embodiment.

The methods of the invention, in addition to enabling the specific killing of

10 telomerase-positive cells, can also be used to prevent transformation of telomerase negative cells to a telomerase positive state. As shown in Example 1, an hTERT promoter sequence can be operably linked to a reporter gene such that activation of the promoter results in expression of the protein encoded by the reporter gene. If, instead of a reporter protein, the encoded protein is toxic to the cell, activation of the promoter leads

15 to cell morbidity or death.

Modifying TERT Promoters by *In vivo* Homologous Recombination: Generating TERT "Knockout" Cells

In another embodiment, the introduced TERT promoter sequence (modified or wild type) can replace or disrupt an endogenous TERT promoter sequence

20 (*e.g.*, gene replacement and "gene knockout," respectively). A newly introduced TERT promoter sequence can be engineered to have greater or lesser transcriptional activity, be responsive to new trans-acting transcriptional modulating agents, and the like.

Disruption of an endogenous TERT promoter sequence typically will decrease or abrogate ("knockout") the transcription of TERT. Therapeutic indications for

25 such TERT promoter activity manipulations are discussed above. In one embodiment, the TERT promoter "knockout" is prepared by deletion or disruption by homologous recombination of the endogenous hTERT promoter. Homologous recombination and other means to alter (and "knockout") expression of endogenous sequences is well known in the art and is described in, *e.g.*, Moynahan (1996) Hum. Mol. Genet. 5:875; Moynahan

30 (1996) Hum. Mol. Genet. 5:875; Baudin (1993) Nucl. Acids Res. 21:3329; Wach (1994) Yeast 10:1793; Rothstein (1991) Methods Enzymol. 194:281; Anderson (1995) Methods Cell Biol. 48:31; Pettitt (1996) Development 122:4149-4157; Ramirez-Solis (1993) Methods Enzymol. 225:855; Thomas (1987) Cell 51:503; Couldrey (1998) Dev. Dyn.

212:284-292). Holzschu (1997) Transgenic Res 6:97-106; U.S. patents 5,464,764; 5,631,153; 5,487,992; 5,627,059, and 5,272,071; WO 91/09955; WO 93/09222; WO 96/29411; WO 95/31560; WO 91/12650.

Vectors useful in TERT gene therapy can be, *e.g.*, viral or nonviral. They

5 may comprise other regulatory or processing sequences. Gene therapy vectors are well known in the art, see, *e.g.*, Lyddiatt (1998) Curr Opin Biotechnol 9:177-85.

As the invention is also directed to methods and reagents for gene replacement therapy (*e.g.*, replacement by homologous recombination of an endogenous TERT gene with a recombinant gene), vectors-specifically designed for integration by

10 homologous recombination comprising TERT promoter sequences are also provided by the invention. Important factors for optimizing homologous recombination include the degree of sequence identity and length of homology to chromosomal sequences. The specific sequence mediating homologous recombination is also important, because integration occurs much more easily in transcriptionally active DNA. Methods and

15 materials for constructing homologous targeting constructs are described by *e.g.*, Mansour (1988) Nature 336: 348; Bradley (1992) Bio/Technology 10:534; U.S. Patent Nos. 5,627,059; 5,487,992; 5,631,153; and 5,464,764.

The invention provides delivery of the expression systems (*e.g.*, gene therapy vectors) of the invention into cells or tissues *in vitro* or ex vivo. For ex vivo

20 therapy, vectors may be introduced into cells, *e.g.*, stem cells, taken from the patient and clonally propagated for autologous transplant back into the same patient; see, *e.g.*, U.S. Patent Nos. 5,399,493 and 5,437,994. Cells that can be targeted for TERT promoter gene therapy aimed at increasing the telomerase activity of a target cell include, but are not limited to, embryonic stem or germ cells, particularly primate or human cells,

25 hematopoietic stem cells (AIDS and post-chemotherapy), vascular endothelial cells (cardiac and cerebral vascular disease), skin fibroblasts and basal skin keratinocytes (wound healing and burns), chondrocytes (arthritis), brain astrocytes and microglial cells (Alzheimer's Disease), osteoblasts (osteoporosis), retinal cells (eye diseases), and pancreatic islet cells (Type I diabetes).

30 In one embodiment , the targeted cells are embryonic stem cells used to generate the non-human transgenic animals (*e.g.*, mice) of the invention, as described herein.

PHARMACEUTICAL COMPOSITIONS

The invention provides pharmaceutical compositions that comprise TERT promoter-containing nucleic acids (*e.g.*, oligo- and poly-nucleotides, expression vectors, gene therapy constructs, etc.) alone or in combination with at least one other agent, such as, *e.g.*, a stabilizing compound, diluent, carrier, cell targeting agent, or another active ingredient or agent. The therapeutic agents of the invention may be administered in any sterile, biocompatible pharmaceutical carrier, including, but not limited to, saline, buffered saline, dextrose, and water. Any of these molecules can be administered to a patient alone, or in combination with other agents, drugs or hormones, in pharmaceutical compositions where it is mixed with suitable excipient(s), adjuvants, and/or pharmaceutically acceptable carriers.

The pharmaceutical compositions of the invention can be administered by any means, such as, *e.g.*, oral, parenteral, and the like. Methods of parenteral delivery include *e.g.*, topical, intra-arterial (*e.g.*, directly to the tumor), intramuscular (IM), subcutaneous (SC), intramedullary, intrathecal, intraventricular, intravenous (IV), intraperitoneal (IP), or intranasal administration. Further details on techniques for formulation and administration may be found in the latest edition of "REMINGTON'S PHARMACEUTICAL SCIENCES" (Maack Publishing Co, Easton PA). See also, *e.g.*, PCT publication WO 93/23572.

Pharmaceutical compositions of the invention include TERT-containing nucleic acids in an effective amount to achieve the intended purpose. "Therapeutically effective amount" or "pharmacologically effective amount" are well recognized phrases and refer to that amount of an agent effective to produce the intended pharmacological result. For example, a therapeutically effective amount is an amount sufficient to treat a disease or condition or ameliorate the symptoms of the disease being treated. Useful assays to ascertain an effective amount for a given application (*e.g.*, a therapeutically effective amount) includes, *e.g.*, to measure the effect on endogenous TERT promoter activity and telomerase activity in a target cell (in the case of, *e.g.*, inhibition therapy). The amount actually administered will be dependent upon the individual to which treatment is to be applied, and will preferably be an optimized amount such that the desired effect is achieved without significant side effects. The therapeutically effective dose can be estimated initially either in cell culture assays or in any appropriate animal model. The animal model is also used to estimate appropriate dosage ranges and routes

of administration in humans. Thus, the determination of a therapeutically effective dose is well within the capability of those skilled in the art.

PRODUCTION OF IMMORTALIZED CELLS, CELL LINES, AND ANIMALS

As described above, as an extension of the various embodiments providing

5   TERT promoter-containing compositions and methods to increase TERT promoter activity, and to thereby increase telomerase expression, thus increasing the proliferative capacity of the cell, the invention also provides immortalized cells, cell lines and animals using the TERT promoter sequences of the invention. As discussed above, most vertebrate cells senesce after a finite number of divisions in culture (*e.g.*, 50 to 100

10   divisions). Certain variant cells, however, are able to divide indefinitely in culture (*e.g.*, HeLa cells, 293 cells) and, for this reason, are useful for research and industrial applications. Usually these immortal cell lines are derived from spontaneously arising tumors, or by transformation by exposure to, *e.g.*, an oncogene, radiation or a tumor-inducing virus or chemical. Unfortunately, a limited selection of cell lines, especially

15   human cell lines representing differentiated cell function, is available. Moreover, many immortal cell lines presently available are characterized by chromosomal abnormalities (*e.g.*, aneuploidy, gene rearrangements, or mutations). Further, many long-established cell lines are relatively undifferentiated (*e.g.*, they do not produce highly specialized products of the sort that uniquely characterize particular tissues or organs). Thus, there is

20   a need for the TERT promoter activating compositions and methods of the invention to generate new immortal cell lines, especially using cells of human origin, where hTERT promoter activating compositions and methods are preferred.

The "immortalized cells" of the invention are not limited to those that proliferate indefinitely, but also include cells with increased proliferative capacity

25   compared to similar cells whose TERT promoter has not been upregulated. Depending on the cell type, increased proliferative capacity may mean proliferation for at least about 50, about 100, about 150, about 200, or about 400 or more generations, or for at least about 3, about 6, about 12, about 18, about 24 or about 36 or more months in *in vitro* culture.

30   Uses for cells with increased proliferative capacity include, *e.g.*, the production of natural proteins and recombinant proteins (*e.g.*, therapeutic polypeptides such as erythropoietin, human growth hormone, insulin, and the like), or antibodies, for which a stable, genetically normal cell line is preferred. Another use is for replacement

of diseased or damaged cells or tissue. For example, autologous immune cells immortalized using an TERT promoter sequence of the invention can be used for cell replacement in a patient after aggressive cancer therapy, *e.g.*, whole body irradiation. Another use for immortalized cells is for *ex vivo* production of "artificial" tissues or

5   organs (*e.g.*, skin) for therapeutic use. Another use for such cells is for screening or validation of drugs, such as telomerase-inhibiting drugs, or for use in production of vaccines or biological reagents. Additional uses of the cells of the invention will be apparent to those of skill.

KARYOTYPE ANALYSIS: DELETIONS, AMPLIFICATIONS, AND
10 ## TRANSLOCATIONS

The present invention further provides methods and reagents for karyotype analysis, gene amplification detection, or other chromosomal analysis using probes comprising the TERT promoter sequences of the invention. In various embodiments, amplifications (*e.g.*, change in copy number), deletions, insertions, substitutions, or

15 changes in the chromosomal location (*e.g.*, translocations) of TERT promoter containing genes are detected. These can be correlated with the presence of a pathological condition or a predisposition to developing a pathological condition (*e.g.*, cancer). Thus, this information can be used in a diagnostic or prognostic manner.

For instance, a translocation event could indicate that activation of TERT

20 expression occurs in some cases by replacing all or part of the TERT promoter with another promoter element (*e.g.*, a non-TERT promoter or enhancer) which directs TERT transcription in an inappropriate manner. Furthermore, the methods and reagents of the invention can be used to inhibit this inappropriate TERT activation.

Determining the chromosomal location of TERT promoter sequence may

25 also be useful for analysis of TERT gene repression in normal somatic cells, for instance, whether the location is part of non-expressing heterochromatin. Nuclease hypersensitivity assays for distinguishing heterochromatin and euchromatin are described, *e.g.*, in Wu (1979) Cell 16:797; Groudine (1982) Cell 30:131; Gross (1988) Ann. Rev. Biochem. 57:159. Methods for analyzing karyotype are well known in the art, and are

30 discussed in detail in related applications   See also, *e.g.*, Pinkel (1988) Proc. Natl. Acad. Sci. USA 85:9138; EPO Pub. No. 430,402; Choo, ed., METHODS IN MOLECULAR BIOLOGY VOL. 33: IN SITU HYBRIDIZATION PROTOCOLS, Humana Press, Totowa, New Jersey, 1994; Kallioniemi (1992) Science 258:818).

SCREENING AND ISOLATING TERT PROMOTER BINDING PROTEINS AND OTHER *TRANS*-ACTING TRANSCRIPTIONAL AGENTS

In addition to the novel TERT promoter sequences and identification of the cis-acting transcriptional regulatory sequences contained therein, the invention

5 provides for novel *in vitro* and cell-based *in vivo* assay systems to screen for TERT promoter binding proteins (trans-acting transcriptional regulatory factors) using the nucleic acids of the invention. Many assays are available that screen for nucleic acid binding proteins and all can be adapted and used with the novel TERT sequences provided by the invention. A few illustrative example are set forth below.

10 One embodiment of the invention provides a method of screening and isolating a TERT promoter binding compound by contacting a TERT promoter sequence of the invention (particularly, an identified cis-acting regulatory sequence) with a test compound and measuring the ability of the test compound to bind the selected nucleic acid. The test compound, as discussed above, can be any agent capable of specifically

15 binding to a TERT promoter activity, including compounds available in chemical (*e.g.*, combinatorial) libraries, a cell extract, a nuclear extract, a protein or peptide. If a TERT transcriptional activating protein is the goal of the search, a cell with telomerase activity is typically chosen.

A variety of well-known techniques can be used to identify polypeptides

20 which specifically bind to TERT promoter, *e.g.*, mobility shift DNA-binding assays, methylation and uracil interference assays, DNase and hydroxy radical footprinting analysis, fluorescence polarization, and UV crosslinking or chemical cross-linkers. For a general overview, see, *e.g.*, Ausubel (chapter 12, DNA-Protein Interactions). One technique for isolating co-associating proteins, including nucleic acid and DNA/RNA

25 binding proteins, includes use of UV crosslinking or chemical cross-linkers, including *e.g.*, cleavable cross-linkers dithiobis (succinimidylpropionate) and 3,3'-dithiobis (sulfosuccinimidyl-propionate); see, *e.g.*, McLaughlin (1996) Am. J. Hum. Genet. 59:561-569; Tang (1996) Biochemistry 35:8216-8225; Lingner (1996) Proc. Natl. Acad. Sci. USA 93:10712; Chodosh (1986) Mol. Cell. Biol 6:4723-4733. In many cases, there

30 is a high likelihood that a specific protein (or a related protein) may bind to an hTERT promoter sequence, *e.g.*, a Myc, NF-kappa B, EF2, Sp1, AP-1 or CAAT box binding site. In these scenarios, where an antibody may already be available or one can be easily generated, co-immunoprecipitation analysis can be used to identify and isolate TERT

promoter-binding, trans-acting factors. The trans-acting factor can be characterized by peptide sequence analysis. Once identified, the function of the protein can be confirmed by methods known in the art, for example, by competition experiments, factor depletion experiments using an antibody specific for the factor, or by competition with a mutant

5   factor.

Alternatively, TERT promoter-affinity columns can be generated to screen for potential TERT binding proteins. In a variation of this assay, TERT promoter subsequences are biotinylated, reacted with a solution suspected of containing a binding protein, and then reacted with a strepavidin affinity column to isolate the nucleic acid or

10   binding protein complex (see, *e.g.*, Grabowski (1986) Science 233:1294-1299; Chodosh (1986) supra). The promoter-binding protein can then be conventionally eluted and isolated. Mobility shift DNA-protein binding assay using nondenaturing polyacrylamide gel electrophoresis (PAGE) is an extremely rapid and sensitive method for detecting specific polypeptide binding to DNA (see, *e.g.*, Chodosh (1986) supra, Carthew (1985)

15   Cell 43:439-448; Trejo (1997) J. Biol. Chem. 272:27411-27421; Bayliss (1997) Nucleic Acids Res. 25:3984-3990).

Interference assays and DNase and hydroxy radical footprinting can be used to identify specific residues in the nucleic acid protein -binding site, see, *e.g.*, Bi (1997) J. Biol. Chem. 272:26562-26572; Karaoglu (1991) Nucleic Acids Res. 19:5293-

20   5300. Fluorescence polarization is a powerful technique for characterizing macromolecular associations and can provide equilibrium determinations of protein-DNA and protein-protein interactions. This technique is particularly useful (and better suited than electrophoretic methods) to study low affinity protein-protein interactions, see, *e.g.*, Lundblad (1996) Mol. Endocrinol. 10:607-612.

25   Proteins identified by these techniques can be further separated on the basis of their size, net surface charge, hydrophobicity and affinity for ligands. In addition, antibodies raised against such proteins can be conjugated to column matrices and the proteins immunopurified. All of these general methods are well known in the art. See,.e.g, Scopes, R. K., Protein Purification: Principles and Practice, 2nd ed., Springer

30   Verlag, (1987).

Transgenic Non-Animals Incorporating TERT Genes

The invention also provides non-human transgenic animals comprising heterologous TERT or recombinant constructs comprising endogenous TERT promoter.

In a preferred embodiment, the transgenic animals of the invention comprise a TERT promoter driving a heterologous gene, such as a reporter gene coding sequence. In a preferred embodiment, an hTERT promoter of the invention is operably linked to a reporter gene in a transgenic mouse. Alternatively, an mTERT promoter is operably

5   linked to a reporter gene in a transgenic mouse. These transgenic animals are very useful as *in vivo* animal models to screen for modulators of TERT transcriptional activity. The introduction of hTERT, mTERT or other TERT promoters into animals to generate transgenic models is also used to assess the consequences of mutations or deletions to the transcriptional regulatory regions.

10   In one embodiment, the endogenous TERT gene in these mice is still functional and wild-type (native) telomerase activity can still exist. A TERT promoter of the invention (*e.g.*, hTERT or mTERT) is used to drive a high level expression of an exogenous TERT construct, the endogenously produced mTERT protein can be competitively replaced with the introduced, exogenous TERT protein. This transgenic

15   animal (retaining a functional endogenous telomerase activity) is preferred in situations where it is desirable to retain "normal," endogenous telomerase function and telomere structure. In other situations, where it is desirable that all telomerase activity is by the introduced exogenous TERT protein, use of an mTERT knockout line (described below) is preferred.

20   . Promoter function, and in a preferred embodiment, hTERT promoter function, can be assessed with these transgenic animals. Alterations of TERT promoters can be constructed that drive TERT or a reporter gene to assess their function and expression pattern and characteristics (the invention also provides constructs and animals and methods for gene expression driven by a TERT promoter by transient transfection).

25   In one embodiment, the TERT promoters and reagents of the invention are used to create mouse cells and transgenic animals in which the endogenous TERT promoter is deleted, modified, supplemented or inhibited. For example, TERT promoter sequences can be deleted, modified or inhibited on either one or both alleles. The cells or animals can be reconstituted with a wild-type or modified TERT promoter, or, in a

30   preferred embodiment, an exogenous TERT in the form of hTERT. Methods for the construction of transgenic animals, particularly trangenic mice, and the selection and preparation of recombinant constructs for generating transformed cells are well known in the art.

Construction of a "knockout" cell and animal is based on the premise that the level of expression of a particular gene in a mammalian cell can be decreased or completely abrogated by introducing into the genome a new DNA sequence (*e.g.*, a TERT or other nucleic acid construct of the invention) that serves to interrupt some portion of

5   the DNA sequence of the gene/promoter to be suppressed. To prevent expression of endogenous promoter, simple mutations that alter or disrupt the promoter can be suitable. To upregulate expression, a native TERT promoter can be substituted with a heterologous or mutated TERT promoter that induces higher levels of transcription, or with multiple copies of trangene TERT promoters. Also, "gene trap insertion" can be used to disrupt a

10   host gene, and mouse embryonic stem (ES) cells can be used to produce knockout transgenic animals, as described herein and, *e.g.*, in Holzschu (1997) Transgenic Res 6: 97-106.

In a preferred embodiment, cell and trangenic animal models express TERT promoter (particularly, hTERT promoter) operably linked to a reporter gene. The

15   cell or animal can be a TERT promoter "knockout" or it can retain endogenous TERT promoter activity. The insertion of the TERT promoter-containing exogenous sequence is typically by homologous recombination between complementary nucleic acid sequences. Thus, the exogenous sequence, which is typically an hTERT or mTERT promoter of this invention, is some portion of the target (*e.g.*, mTERT) gene to be modified, such as

20   exonic, intronic or transcriptional regulatory sequences, or any genomic sequence which is able to affect the level of the target gene's expression; or a combination thereof. The construct can also be introduced into other (*i.e.*, non-mTERT gene) locations in the genome. Gene targeting via homologous recombination in pluripotential embryonic stem cells allows one to modify precisely the genomic sequence of interest.

25   The exogenous sequence is typically inserted in a construct, usually also with a marker gene to aid in the detection of the knockout construct and/or a selection gene. The construct can be any of a variety of expression vectors, plasmids, and the like, as described above. The knockout construct is inserted in a cell, typically an embryonic stem (ES) cell, using a variety of techniques, as described above. The insertion of the

30   exogenous DNA usually occurs by homologous recombination. The resultant transformed cell can be a single gene knockout (*i.e.*, only one of the two copies of the endogenous TERT promoter has been modified) or a double gene knockout. The knockout construct can be integrated into one or several locations in the cell's genome

due to the random nature of homologous recombination events; however, the recombination does occur between regions of sequence complementarity. Typically, less than one to five percent of the ES cells that take up the knockout construct will actually integrate exogenous DNA in these regions of complementarity; thus, identification and

5 selection of cells with the desired phenotype is usually necessary and a selection or marker sequence is usually incorporated into the construct for this purpose. Cells which have incorporated the construct are selected for prior to inserting the genetically manipulated cell into a developing embryo; for example, the cells are subjected to positive selection (using G418, for example, to select for neomycin-resistance) and

10 negative selection (using, for example, FIAU to exclude cells lacking thymidine kinase). A variety of selection and marker techniques are well known in the art, *e.g.*, antibiotic resistance selection or beta-galactosidase marker expression can be used and are further described herein.

After selection of manipulated cells with the desired phenotype, *i.e.*,

15 complete or partial inability to express endogenous TERT promoter, or, expression of the exogenous TERT promoter (as hTERT promoter activity) the cells are inserted into a mouse embryo. Insertion can be accomplished by a variety of techniques, such as microinjection, in which about 10 to 30 cells are collected into a micropipet and injected into embryos that are at the proper stage of development to integrate the ES cell into the

20 developing embryonic blastocyst, at about the eight cell stage, which for mice is about 3.5 days after fertilization. The embryos are obtained by perfusing the uterus of pregnant females. After the ES cell has been introduced into the embryo, it is implanted into the uterus of a pseudopregnant foster mother, which is typically prepared by mating with vascectomized males of the same species. In mice, the optimal time to implant is about

25 two to three days pseudopregnant. Offspring are screened for integration of the TERT nucleic acid sequences and the modified promoter activity phenotype. Offspring that have the desired phenotype are crossed to each other to generate a homozygous knockout. If it is unclear whether germline cells of the offspring have modified promoter, they can be crossed with a parental or other strain and the offspring screened for heterozygosity of

30 the desired trait. The heterozygotes can be crossed with each other to produce mice homozygous for modified TERT genomic sequence. While the above described methodology describes a typical protocol, any technique can be used to create, screen for, propagate, a knockout animal, particularly, an mTERT knockout mice, *e.g.*, see Bijvoet

(1998) Hum. Mol. Genet. 7:53-62; Moreadith (1997) J. Mol. Med. 75:208-216; Tojo
(1995) Cytotechnology 19:161-165; Mudgett (1995) Methods Mol. Biol. 48:167-184;
Longo (1997) Transgenic Res. 6:321-328; U.S. Patents Nos. 5,616,491 (Mak, et al.);
5,464,764; 5,631,153; 5,487,992; 5,627,059; 5,272,071; and, WO 91/09955, WO

5   93/09222, WO 96/29411, WO 95/31560, and WO 91/12650. Thus, the invention
provides for the use of the TERT promoter sequence-containing reagents of the invention
to produce "knockout" mouse cells and animals, trangenic animals, and their progeny.
These cells and animals can be further reconstituted with wild type or modified
endogenous mTERT promoter or exogenous TERT promoter, such as hTERT.

10

It is understood that the examples and embodiments described herein are
for illustrative purposes only and that various modifications or changes in light thereof
will be suggested to persons skilled in the art and are to be included within the spirit and
purview of this application and scope of the appended claims.

15

EXAMPLES

Example 1:   Cloning of Lambda Phage Gphi5 and Characterization of hTERT Genomic Sequences

The following example details the cloning of the human hTERT promoter.

20   *Lambda Phage Gphi5*

A human genomic DNA library was screened by PCR and hybridization to
identify a genomic clone containing hTERT RNA coding sequences. The library was a
human fibroblast genomic library made using DNA from WI38 lung fibroblast cells
(Stratagene, Cat # 946204). In this fibroblast library, partial Sau3AI fragments were

25   ligated into the XhoI site of a commercial phage cloning vector, Lambda FIX(r)II Vector
(Stratagene, San Diego, CA), with insert sizes ranging from approximately 9 kilobases
(kb) to 22 kb.

The genomic library was divided into pools of 150,000 phage each. Each
pool screened by nested PCR, with the outer primer pair TCP1.52 & TCP1.57; inner pair

30   TCP1.49 & TCP1.50, see Table 1. These primer pairs span a putative intron in the
genomic DNA of hTERT and ensured the PCR product was derived from a genomic
source and not from contamination by the hTERT cDNA clone. Positive pools were
further subdivided until a pool of 2000 phage was obtained. This pool was plated at low

density and screened via hybridization with a DNA fragment encompassing a subset of hTERT cDNA, generated by restriction digest with SphI and EcoRV.

Two positive clones were isolated and rescreened via nested PCR as described above. At rescreening, both clones were positive by PCR. One of the lambda phage clones (designated "Gphi5" or G (5) was digested with NotI, revealing an insert size of approximately 20 kb. Subsequent mapping indicated the insert size was 15 kb and that phage Gphi5 contains approximately 13 kb of DNA upstream from the transcriptional start site (upstream from the cDNA sequence). Phage Gphi5 was mapped by restriction enzyme digestion and DNA sequencing. The resulting map is shown in Figure 1.

Isolating, Subcloning and Sequencing the Genomic hTERT Insert

The phage DNA was digested with NcoI. This fragment was cloned into the plasmid pBBS167. The resulting subclones were screened by PCR to identify those containing sequences corresponding to the 5' region of the hTERT cDNA. A subclone (plasmid "pGRN140") containing a 9 kb NcoI fragment (with hTERT gene sequence and about 4 to 5 kb of lambda vector sequence) was partially sequenced to determine the orientation of the insert. pGRN140 was digested using SalI to remove lambda vector sequences, the resulting plasmid (with removed lambda sequences) designated pGRN144. The pGRN144 insert was then sequenced.

A NotI fragment (SEQ ID NO:1) from lambda Gphi5 (containing the complete approximately 15 kbp genomic insert including the hTERT gene promoter region) was inserted in the NotI site of plasmid pBBS185. Two plasmids were isolated with their respective inserts oriented in opposite directions. One resulted in the insert oriented with the hTERT open reading frame (ORF) in the same orientation as the plasmid's Lac promoter, designated pGRN 142; the second, pGRN 143. pGRN142 has been deposited in GenBank with the Accession Number PGRN142.INS AF121948 (see National Center for Biotechnology Information at http://www.ncbi.nlm.nih.gov/Web/Search/index.html).

The insert in pGRN 142 was sequenced; the results of which are provided as SEQ ID NO:1. In SEQ ID NO:1, the genomic insert begins at residue 44 and ends at residue 15375. The hTERT cDNA start site is at residue 13490. The hTERT ATG codon is at residue 13545. As indicated in Figure 1, Alu sequence elements are located 1700 base pairs upstream of the hTERT cDNA 5' end.

Example 2: TERT Promoter-Driven Reporter Constructs

This example describes the construction of plasmids in which reporter genes are operably linked to hTERT promoter sequences of the invention. This also illustrates how the TERT promoter sequence of the invention can analogously be operatively linked to heterologous sequences, such as polypeptide coding sequences, for expression in cells and tissues *in vitro* and *in vivo* and transgenic animals.

hTERT-linked reporter vectors of the invention have numerous uses, including, *e.g.*, identification of specific cis-acting sequences and trans-acting transcriptional regulatory factors. Importantly, these hTERT-containing reporter constructs can be used for the screening of agents capable of modulating (*e.g.*, activating or inhibiting) hTERT transcription (*e.g.*, drug screening). These studies can be *in vitro* and *in vivo*.

A number of reporter genes, *e.g.*, firefly luciferase, beta-glucuronidase, beta-galactosidase, chloramphenicol acetyl transferase, and GFP and the like, are known in the art and can be operably linked to hTERT promoter. In this example, the human secreted alkaline phosphatase (SEAP; ClonTech) was used. The SEAP reporter gene encodes a truncated form of the placental enzyme which lacks the membrane anchoring domain, thereby allowing the protein to be secreted efficiently from transfected cells. Levels of SEAP activity detected in the culture medium have been shown to be directly proportional to changes in intracellular concentrations of SEAP mRNA and protein. The chemiluminescence-based SEAP assay is about 10-fold more sensitive than similar assays using firefly luciferase as the reporter enzyme. The SEAP activity can also be assayed with a fluorescent substrate, which provides sensitivity comparable to luciferase. See, *e.g.*, Berger (1988) Gene 66:1; Cullen (1992) Meth. Enzymol. 216:362; Yang (1997) Biotechniques 23:1110-1114.

hTERT 5' Upstream and Intronic Sequences have "Promoter" Activity

Experiments with reporter constructs comprising various hTERT sequences of the invention identified cis-acting regions with "promoter" transcriptional activating activity in both 5' upstream and intronic sequences. In brief, four constructs, pGRN148, pGRN150, "pSEAP2 basic" (no promoter sequences = negative control), and "pSEAP2 control" (contains the SV40 early promoter and enhancer) were constructed (see also details below) and transfected in triplicate into mortal and immortal cells. Plasmid pGRN148 was constructed as illustrated in Figure 3. Briefly, a Bgl2-Eco47III

fragment from pGRN144 (described above) was digested and cloned into the BglII-NruI site of pSeap2Basic (Clontech, San Diego, CA).

A second reporter-promoter, plasmid pGRN150 was made by inserting the BglII-FspI fragment from pGRN144 into the BglII-NruI sites of pSEAP2. Plasmid

5   pGRN173 was constructed by using the EcoRV-StuI fragment from pGRN144. This makes a promoter reporter plasmid that contains the promoter region of hTERT from approximately 2.5 kb upstream from the start of the hTERT ORF to just after the first intron in the coding region. The initiating Met was mutated to Leu, so that the second ATG following the promoter region would be the initiating ATG of the SEAP ORF.

10   Use of the intronic sequence allows identification of regulatory sequences that may be present in the intron (the invention provides transcriptional regulatory sequences from any portion of the hTERT genomic sequence). In addition to the hTERT derived pSEAP reporter constructs, a positive control vector and a negative control vector were used. The negative control (pSEAP2-Basic) is necessary to determine the

15   background signal associated with the DNA backbone of the vector. A positive control is necessary to confirm transfection and expression of exogenous DNA and to verify the presence of active SEAP in the culture media. The positive control is the pSEAP2-Control vector (Clontech) which contains the SEAP structural gene under transcriptional control of the SV40 promoter and enhancer.

20   Three constructs, the control, pGRN148 (which include hTERT 5' promoter sequences) and pGRN150, were transfected into a mortal cell line, BJ cells, a human foreskin fibroblast line; see, *e.g.*, Feng (1995) Science 269:1236; and an immortal cell line, the human embryonic kidney line 293; see, *e.g.*, Graham (1977) J. Gen. Virol. 36:59. All transfections were done in parallel with the two control plasmids.

25   In immortal cells, pGRN148 and pGRN150 constructs appear to drive SEAP expression as efficiently as the pSEAP2 positive control (containing the SV40 early promoter and enhancer). In contrast, in mortal cells only the pSEAP2 control gave detectable activity. Similar results were obtained using another normal cell line (RPE, or retinal pigmental epithelial cells, see, *e.g.*, Aronson (1983) *In vitro* 19:642-650). In RPE

30   cells transfected with pGRN150, the hTERT promoter region was inactive while the pSEAP2 control plasmid was active. These results indicate that, as expected, hTERT promoter sequences are active in tumor cells but not in mortal cells.

Identification of the Tissue Specificity Elements of the hTERT Promoter

           The hTERT DNA promoter sequences were cloned into the pSEAP2-Basic transcription reporter vector (Clontech) to generate the plasmids pGRN 148, 150, 175, 176, 181,184, 261, 262, and 319. Summarized below are details of the promoter plasmid

5   construction (nucleotide numbers refer to the number of nucleotides upstream of the translation initiation site at 13545 of SEQ ID NO:1):

pEGFP-1. *Vector from Clontech containing the "Enhanced Green Flourescent Protein".

pGRN140. *NCO1 fragment containing hTERT upstream sequences and the first intron of hTERT from lambdaGPhi5 into the NCO1·site of a pBBS167 (varient of pUC19

10   cloning vector with MCS, *e.g.*

ATGACCATGATTACGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGTCGA
CCTGCAGGCATGCCCATGGCAGGCCTCGCGCGCGAGATCTCGGGCCCAATCG
ATGCCGCGGCGATATCGCTCGAGGAAGCTTGGCACTGGCC (SEQ ID NO:3) , ·

and a chloramphenicol sensitive gene between the F1ori and the Amp gene in the

15   opposite orientation from the Amp gene). The fragment is oriented so that the hTERT sequences are in the same direction as the Lac promoter.

pGRN144. described above; SalI deletion of pGRN140 to remove phage (lambda) sequences.

pGRN148: *BGL2-ECO47III fragment from pGRN144 containing hTERT upstream

20   sequences (from position -51 to -2482) into the BGL2-NRU1 sites of pSEAP2-Basic to make a hTERT promoter/reporter plasmid.

pGRN150: *BGL2-FSP1 fragment from pGRN144 containing 2447nt of hTERT upstream sequences (from position -36 to -2482) into the BGL2-NRU1 sites of pSEAP2 to make a hTERT promoter/reporter plasmid.

25   pGRN175: *APA1(Klenow blunt)-SRF1 religation of pGRN150 to delete most of the hTERT upstream sequences. This makes a promoter/reporter plasmid that uses 82 nucleotides of hTERT upstream sequences (from position -36 to -117).

pGRN176: *PML1-SRF1 religation of pGRN150 to delete most of the hTERT upstream sequences. This makes a promoter/reporter plasmid that uses 204 nucleotides of hTERT

30   upstream sequences (from position -36 to -239).

pGRN181: *APA1 digestion and religation of pGRN150 to delete all APA1 sites but one. This makes a promoter/reporter plasmid that comprises from -36 to -114 and -1076 to -2482 of the hTERT upstream sequences.

pGRN184: *XBA1(partial, Klenow fill)-ECOR1 digest and religation of pGRN150 to make a deletion of the hTERT promoter sequences. This makes a promoter/reporter plasmid that expresses a region from -1391 to -2484 of the hTERT upstream sequences.

pGRN213. *FSP1 fragment containing the CatS gene and the F1 ORI plus part of the

5 AmpR gene into the FSP1 sites of pSEAP2-Basic such that the orientation reconstructs the AmpR gene.

pGRN244: *SAL1-NOT1 fragment from pSEAP2-Basic containing the SEAP region · into the SAL1-NOT1 sites of pEGFP-1. This modification adds a selectable marker to the vector.

10 pGRN245: *SAL1-NOT1 fragment from pGRN176 containing the hTERT-promoter/SEAP region into the SAL1-NOT1 sites of pEGFP-1. This modification adds a dominant selectable marker to the vector.

pGRN246: *SAL1-NOT1 fragment from pGRN176 containing the hTERT-promoter/SEAP region into the SAL1-NOT1 sites of pEGFP-1. This modification adds a

15 dominant selectable marker to the vector.

pGRN248 *SAL1-NOT1 fragment from pGRN175 containing the hTERT promoter/SEAP region into the SalI-NotI sites of pEGFP-1. This modification adds a dominant selectable marker to the vector.

pGRN259. *in vitro mutagenesis using RA94

20 (CCCGGCCACCCCCGCGAattCGCGCGCTCCCCGCTGC) (SEQ ID NO:4) to introduce an EcoRI site at the initiating met of hTERT in pGRN144. This provides hTERT u=sequences from +1 to -2482 that can be cloned into a vector using EcoRI and BglII.

pGRN260. *in vitro mutagenesis using RA91

25 (TTGTACTGAGAGTGCACCATATGCGGTGTGcatgcTACGTAAGAGGTTCCAACT TTCACCATAAT) (SEQ ID NO:5) to delete several sites from the Chloramphenicol region of pGRN213 to create a variant, more useful, MCS. This creates a Mutagenesis version of pSEAP2-Basic with more unique cloning sites in it's MCS.

pGRN261: *BGL2-ECOR1 fragment from pGRN259 containing hTERT upstream

30 sequences into the BGL2-ECOR1 sites of pSEAP2-Basic. This makes a promoter/reporter expression plasmid that contains from +1 to -2482 of the hTERT upstream sequences.

pGRN262: *BGL2-ECOR1 fragment from pGRN259 containing hTERT upstream sequences into the BGL2-ECOR1 sites of pGRN260. This makes a promoter/reporter

expression and mutagenesis plasmid that contains from +1 to -2482 of the hTERT upstream sequences.

pGRN294. *BbsI-XhoI fragment from pGRN142 containing hTERT upstream sequences from -1667 to -3278 into the BbsI-XhoI sites of pGRN259. This makes a vector

5   containing the genomic upstream region for hTERT from +1 to -3278 that can be cloned with EcoRI and XhoI.

pGRN295: *ECOR1-XHO1 fragment from pGRN294 containing from +1 to -3282 of hTERT upstream sequences into the ECOR1-XHO1 sites of pGRN260. This makes a SEAP promoter/reporter/mutagenesis plasmid:·

10   pGRN296: *ECOR1-XHO1 fragment from pGRN294 containing from +1 to -3282 of the hTERT upstream sequences into the ECOR1-XHO1 sites of pSEAP2-Basic. This makes a SEAP promoter/reporter plasmid.

pGRN297. *RA96 (AATTGCGAAGCTTACG) (SEQ ID NO:6) and RA97 (AATTCGTAAGCTTCGC) (SEQ ID NO:7) annealed to make an oligo linker into the

15   ECOR1 sites of pGRN259 replacing the ECOR1 fragment of the intron-exon region of pGRN259.

pGRN299: *XHO1-HIND3 fragment from pGRN298 containing from +1 to -3282 of the hTERT upstream sequences into the XHO1-HIND3 sites of pGL2-Basic. This makes a Luciferase promoter/reporter plasmid with about 3.3Kb of hTERT promoter sequences.

20   pGRN300: *XHO1-SAC1 fragment from pGRN142 containing hTERT upstream sequences into the XHO1-SAC1 sites of pGRN299 such that the resulting construct contains from +1 to -5124 of the hTERT upstream sequences. This creates an hTERT promoter/reporter construct using Luciferase as a reporter.

pGRN310: *SAC1 fragment from pGRN142 containing hTERT upstream sequences into

25   the SAC1 site of pGRN300 such that the resulting construct contains +1 to -7984 of the hTERT upstream sequences. This creates an hTERT promoter/reporter construct using Luciferase as a reporter.

pGRN311. *SPE1 fragment from pGRN142 containing from -4773 to -13501 of the hTERT upstream sequences into the SPE1 site of pGRN300 such that the orientation

30   reconstructs the genomic region. This makes a Luciferase promoter reporter plasmid that contains the entire pGRN142 upstream genomic region of hTERT plus a 365bp region of genomic DNA from the middle of the 13.5Kb genomic region repeated upstream of the T7 promoter.

pGRN312: *BGL2-FSP1 fragment from pGRN144 into the BGL2-HIND3 (Klenow
filled) sites of pGL2-Basic. This makes a Luciferase promoter/reporter version of
pGRN150.

pGRN313: *KPN1-NOT1 digested pGRN311 blunted with T4 polymerase and religated.

5   This makes a Luciferase promoter/reporter plasmid using from +1 to -13501 of the
hTERT upstream sequences.

pGRN316: *oligo RA101 (5'- TAGGTACCGAGCTCTTACGCGTGC
TAGCCCCACGTGGCGGAGGGACTGGGGACCCGGGCA-3') (SEQ ID NO:8) used
for *in vitro* mutagenesis to delete the genomic sequence from pGRN262 between the

10   SRF1 site and the first PML1 site. This makes a promoter- reporter plasmid containing
hTERT upstream sequences from +1 to -239.

pGRN317: *oligo RA100 (5'-TAGGTACCGAGCTCTTACGCGTG
CTAGCCCCTCGCTGGCGTCCCTGCACCCTGGGAGCGC-3') (SEQ ID NO:9) used
for *in vitro* mutagenesis to delete the genomic sequence from pGRN262 between the

15   SRF1 site and next to the last APA1 site. This makes a promoter -reporter plasmid
containing hTERT upstream sequences from +1 to -397.

pGRN319: *RA107 (5'-CGTCCTGCTGCGCACtcaGGAAGCCCTGGCCCC-3') (SEQ
ID NO:10) used for *in vitro* mutagenesis to inactivate the 'B' class E-box just proximal to
the hTERT initiating met in pGRN262. This changes the CACGTG (SEQ ID NO:11) to

20   CACTCA (SEQ ID NO:12). Also COD1941 (5'-GATGAATGCTCATGATTCCG
TATGGCA-3') (SEQ ID NO:13) was used to switch from CatR to CatS introducing a
BSPH1 site and COD2866 (5'-CAGCATCTTTTACTTTCACCAGCGTTTCTG
GGTGCGCAAAAACAGGAAGGCAAAATGCC-3') (SEQ ID NO:14) was used to
select from AmpS to AmpR introducing an FSP1 site. In summary, pGRN319 carries a

25   mutation in the E-box.

pGRN350: *RA104 (5'- TAGGTACCGAGCTCTTACGCGTGC
TAGCCCCTCCCAGCCCCTCCCCTTCCTTTCCGCGGC-3') (SEQ ID NO:15) used for
in vitro mutagenesis to delete the genomic sequence from pGRN262 between the SRF1
site and the last APA1 site before the ATG of the hTERT open reading frame (orf).

30   pGRN351: *SAC2 fragment from pGRN319 into the SAC2 sites of pGRN350 such that
the SEAP orf is recreated. This makes a "deactivated E-box" version of pGRN350.

pGRN352: *RA122 (5'- GACCGCGCTTCCCACtcaGCGGAG GGACTGGGG-3')
(SEQ ID NO:16) used for *in vitro* mutagenesis to "deactivate" the penultimate class "B"
E-box before the translation start site of hTERT.

The pSEAP2-Basic plasmid lacks eukaryotic promoter and enhancer
5   sequences. This vector contains the SV40 late polyadenylation signal inserted
downstream of the SEAP coding sequences to ensure proper and efficient processing of
the transcript in eukaryotic cells. It also contains a synthetic transcription blocker (TB),
composed of adjacent polyadenylation and transcription pause sites to reduce background
transcription. As noted above, the SEAP reporter gene encodes a truncated form of the
10 placental enzyme which lacks the membrane anchoring domain, thereby allowing the
protein to be efficiently secreted from transfected cells.

Levels of SEAP activity detected in the culture medium have been shown
to be directly proportional to changes in intracellular concentrations of SEAP mRNA.
The chemiluminescent SEAP substrate CSPDTM (Clontech) was used to detect secreted
15 SEAP. Use of this substrate enables monitoring of the expression of the SEAP reporter
gene through simple, sensitive, nonradioactive assays of secreted phosphatase activity.
This chemiluminescent assay can detect as little as 10-13 g of SEAP protein. The assay is
linear over a 104 fold range of enzyme concentrations. This makes the assay (and these
vectors) particularly well-suited for comparative analyses.

20 As above, in addition to the hTERT derived pSEAP reporter constructs, a
positive control vector (pSEAP2-Control vector) and a negative control vector (pSEAP2-
Basic) were used. The promoter constructs (pGRN 150, 175,176) and the control vectors
were transfected into immortal (HEK 293) and mortal (BJ fibroblast, RPE, HUVEC) cells
48-72 hours after transfection. The culture media was collected and assayed for SEAP
25 activity. The SEAP activity was detected using the chemiluminescent assay from
CLONTECH, Great EscAPeTM SEAP Chemiluminescence Kit, according to the
manufacturer's protocol. The transfections were performed in triplicate. The culture
media from each transfection was collected after 48-72 hours and assayed in triplicate.
The background values obtained by transfection of the negative control (pSEAP2-Basic)
30 vector was subtracted from the values obtained with the test constructs. The average of
nine measurements was used and plotted for each of the constructs.

Experimental Results in Immortal and Mortal Cell Lines

The results of the assays show that while the hTERT promoter constructs are capable of driving the expression of the reporter SEAP gene in immortal cells, the same constructs are silent in all mortal cells tested. The pSEAP2-Control vector however

5 is active in all cell types regardless of their mortal or immortal status and the pSEAP2-Basic vector is silent in all cells assayed.

hTERT Promoter Driving Thymidine Kinase Expression In vitro

The invention provides constructs comprising heterologous coding sequences operably linked to hTERT promoter sequences. In one embodiment, hTERT

10 coding sequences are operably linked to Herpes simplex virus thymidine kinase ("HSV-TK") coding sequences. HSV-TK is an enzyme that is capable of converting innocuous prodrugs, _e.g._ ganciclovir, into toxic metabolites that interfere with the cellular replication of proliferating cells (_e.g._, cancer cells, which have active hTERT promoter activity). Controlling thymidine kinase (TK) expression by subordinating it to the hTERT promoter

15 restricts TK expression to cells where the hTERT promoter is normally active, _i.e._, tumor cells and other proliferating (_e.g._, immortalized) cells. This prevents TK expression in "normal" cells, where the hTERT promoter is usually silent.

The ability of the hTERT promoter to specifically drive the expression of the TK gene in tumor cells was tested using a variety of constructs: One construct,

20 designated pGRN266, contains an EcoRI-FseI PCR fragment with the TK gene cloned into the EcoRI-FseI sites of pGRN263. pGRN263, containing approximately 2.5 kb of hTERT promoter sequence, is similar to pGRN150, described above, but contains a neomycin gene as selection marker. pGRN267 contains an EcoRI-FseI PCR fragment with the TK gene cloned into the EcoRI-FseI sites of pGRN264. pGRN264, containing

25 approximately 210 bp of hTERT promoter sequence, is similar to pGRN176, described above, but contains a neomycin gene as selection marker. pGRN268 contains an EcoRI-XbaI PCR fragment with the TK gene cloned into the EcoRI-XbaI (unmethylated) sites of pGRN265. pGRN265, containing approximately 90 bp of hTERT promoter sequence, is similar to pGRN175, described above, but contains a neomycin gene as selection marker.

30 These hTERT promoter/TK constructs, pGRN266, pGRN267 and pGRN268, were re-introduced into mammalian cells and TK/+ stable clones (and/or mass populations) were selected. Ganciclovir treatment _in vitro_ of the TK/+ cells resulted in selective destruction of all tumor lines tested, including 143B, 293, HT1080, Bxpc-3,

DAOY and NIH3T3. Significantly, ganciclovir treatment had no effect on normal BJ cells. This clearly demonstrates the tumor-specificity of all three hTERT promoter fragments used in these experiments.

Example 3: Direct *In vivo* hTERT Promoter Suicide Gene Therapy

5   The invention provides reagents and methods for treating diseases involving unwanted cell proliferation by *in vivo* gene therapy. To demonstrate the efficacy of this aspect of the invention, the reagents of the invention were used to treat cancer (of human origin) in an art-accepted animal model. A human cancer cell, the osteosarcoma cell line 143B, which normally expresses the telomerase gene, was

10   transfected with a plasmid containing the TK gene driven by the hTERT promoter.

Specifically, sequences -36 to -2482 upstream of the translation start site of SEQ ID NO:1 were used to drive the TK gene. The plasmid also contained the neomycin phosphotransferase gene. After transfection of cells with the plasmid, G418 resistant clones expressing TK were selected. Two hundred thousand of the parental or

15   TK expressing 143B cells were injected subcutaneously in the flank of Balb/c nude (nu/nu) mice to establish tumors. Four to 11 days after tumor implantation the mice were injected IP with 75 mg/kg ganciclovir (GCV) or saline twice daily. Tumor growth was monitored every 3-4 days. When GCV was administered either at 4 or at 11 days post tumor implantation to these tumor bearing animals, TK mediated cell lysis and retarded

20   tumor growth was observed. Such inhibition of tumor cell growth is not observed when saline is administered or if the parental 143B tumor (143BP) is treated with either saline or GCV. Forty-five days after tumor implantation, only the animals implanted with the TK+ 143B clone and treated with GCV showed 100% survival. In the other groups all but one animal died from massive tumor burden.

25   These data indicate that the hTERT promoter is sufficient to drive TK gene expression both *in vivo*. It also shows that the reagents and methods of the invention can be used to promote tumor regression *in vivo* in animals carrying pre-established tumors; *i.e.*, the reagents of the invention can be used to treat cancer patients with pre-existing tumors.

30   **Example 4: Oncolytic Viruses Under Control of the hTERT Promoter**

As discussed above, the invention provides "conditionally replicating" oncolytic virus constructs (*e.g.*, gene therapy vectors) in which hTERT promoter sequences of the invention are operably linked to essential virally encoded genes. Use of

hTERT promoter sequences of the invention ensures the virus will only be productively expressed in cells with telomerase activity. Thus, constructs can be used therapeutically to lyse only cells that express telomerase, such as immortal or cancer cells. Proliferation of the virus and its cytopathic effects is thus restricted to tumor cells. Details of the construction of an exemplary hTERT promoter driven, conditionally replicating oncolytic virus follows. In this embodiment, the hTERT promoter replaces the normal E1a promoter to create a virus which will only replicate in telomerase expressing cells.

Plasmid pBR/ITR/549-ClaI containing nucleotides 1-356 (Ad2 ITR and packaging signals) and 549-920 (a portion of the E1a coding sequence) of Adenovirus 2 (Ad2) linked using a polylinker was built using standard molecular biology procedures in the bacterial plasmid pBR322. In pBR/ITR/TB+phTERT176-E1A and pBR/ITR/TB+phTERT316-E1A, the normal E1a promoter (Ad2 357-548) has been replaced with the hTERT promoter. Ad2 sequences from 916-10680 are added to these plasmids to recreate the expression elements of the 5' end of the virus.

These plasmids (pBR/ITR/TB+phTERT176-10680 and pBR/ITR/TB+phTERT316-10680) are transfected into a telomerase expressing human cell line along with an adenoviral DNA fragment containing Ad2 sequences 10681-35937. Recombinant plaques are scored and selected 7-21 days post transduction. The hTERT promoter E1a containing Ad2 is propagated and produced for use employing standard schemes for recombinant Ad2 amplification and manufacturing. (Graham and Prevec, 1991, in Methods in Molecular Biology, Chapter 11, Ed E.J. Murray, The Human Press Inc., Clifton, NJ.; Kanegae et al., Jpn J Med Sci Biol, 1994, 47(3):157-66). Because the E1a gene is driven by the hTERT promoter, which is not normally expressed by most somatic cells, recombinant Ad2 genome will only replicate and be packaged into virus particles in cells expressing telomerase (*i.e.*, immortal cells, tumor cells).

Example 5: hTERT Promoter Sequences Driving an Alkaline Phosphatase Reporter Gene for High Throughput Screening.

The invention provides constructs and promoter-based assays to identify small molecule activators and/or repressors of hTERT and telomerase activity. To this end, fragments of the hTERT promoter were cloned into plasmids expressing a secreted form of alkaline phosphatase and a selection marker. The SEAP constructs described above (pGRN244, pGRN245, pGRN246 and pGRN248) were re-introduced into normal human cells and into immortal cell lines. After selection of stable clones having

integrated the hTERT promoter/SEAP constructs, RT-PCR was used to determine the levels of SEAP mRNAs. In 293 cells, the levels of SEAP mRNA were elevated and comparable to the levels of endogenous hTERT, whereas in BJ cells, the levels of SEAP mRNA were virtually undetectable and closely matched the levels of the endogenous

5   hTERT in these cells.

These results indicate that hTERT promoter/SEAP constructs can be used to engineer cells suitable for promoter-based assays and to screen for chemical and/or biological activators and/or repressors of telomerase in normal and tumor cells. pGRN244, pGRN245, pGRN246 and pGRN248 were re-introduced into BJ and 293 cells.

10   SEAP activity and mRNA levels were determined in these cells as criteria for clone selection. Several 293 and BJ lines were selected and two BJ/pGRN245 clones were expanded for high throughput screening. These constructs were also introduced into IDH4 cells, which are immortal lung fibroblasts that express the SV40 large T antigen under the control of the dexamethasone-inducible MMTV promoter. IDH4 cells are

15   telomerase positive and proliferate in the presence of dexamethasone. However, these cells can be induced into a senescent, telomerase negative stage after dexamethasone removal. Upon re-addition of dexamethasone, the cells return to an immortal phenotype and re-activate telomerase.

pGRN244, pGRN245, pGRN246 and pGRN248 were transfected into

20   IDH4 cells. SEAP activity was shown to parallel telomerase activity in the different clones, whereas no significant fluctuation of SEAP activity was observed with the control plasmid. These results indicate that a fragment of approximately 2.5 kb of hTERT promoter sequence (pGRN245) contains sufficient sequence elements to support both activation and repression in response to proliferation and/or growth arrest stimuli that

25   control telomerase activity in IDH4 cells. Two clones, ID245-1 and ID245-16 whose SEAP profile closely matched telomerase activity during drug treatment, were selected and expanded for high throughput screening of small molecule activators of telomerase.

Example 6: hTERT Promoter Sequences Driving a β-galactosidase Reporter Gene to Identify Biological Regulators of hTERT and Telomerase activity.

30   The invention also provides constructs and promoter-based assays to identify biological modulators of hTERT and telomerase activity. An exemplary construct of this aspect of the invention is pGRN353 containing a BglII-HindIII fragment from pGRN297 with approximately 2.5 kb of hTERT promoter sequences cloned into the

BglII-HindIII sites of ß-gal-Basic (Clontech). pGRN353 or similar constructs are re-introduced into BJ cells by co-transfection with a plasmid containing a hygromycin gene as selection marker. Clonal cell lines and/or mass populations are established and used to screen retroviral based cDNA libraries for genes or fragments of genes that can activate

5 the hTERT promoter. pGRN353 or similar constructs are also re-introduced into 143B and 293 cells to screen retroviral libraries to identify sequences that can repress the hTERT promoter.

Example 7: Identifying Trans-Acting Transcriptional Regulatory Elements

The promoter-reporter (and other) vectors of the invention are also used to

10 identify trans-acting transcriptional regulatory elements. As noted supra, plasmids in which reporter genes are operably linked to hTERT promoter sequences are extremely useful for identification of trans-acting transcriptional modulatory agents and for the screening of potential hTERT promoter-modulating drugs (including biological agents and small molecules, as discussed above). Both transient and stable transfection

15 techniques can be used. In one embodiment, stable transformants of pGRN148 are made in telomerase negative and telomerase positive cells by cotransfection with a eukaryotic selectable marker (such as neo), according to Ausubel, supra.

The resulting cell lines are used for screening of putative telomerase trans-acting (*e.g.*, promoter sequence binding) transcriptional modulatory agents, *e.g.*, by

20 comparing hTERT-promoter-driven expression in the presence and absence of the test compound (the putative trans-acting transcriptional modulating agent). Additional promoter-reporter vectors (including the constructs described herein, as variations thereof) are similarly used to identify and isolate trans-acting factors binding to cis-acting transcriptional regulatory elements, such as, Myc, Sp1, TATA box binding protein, AP-1,

25 CREB, CAAT binding factor and factors binding to hormone response elements (*e.g.*, GRE). The identification and isolation of such trans-acting regulatory sequences provide for further methods and reagents for modulating the transcription and translation of telomerase.

Example 8: c-Myc acts as a Potent Activator of the TERT Promoter by Direct
30 ### Interaction with Cis-Acting Regulatory Sequences

Use of recombinant constructs comprising TERT promoter sequences of the invention has, for the first time, demonstrated that c-Myc acts as a potent activator of telomerase activity by direct interaction with cis-acting regulatory sequences in the TERT

promoter. Significantly, the studies of the invention also show that transcriptional activation of the hTERT promoter by c-Myc can be abrogated by deletion or mutation of a single cis-acting regulatory sequence, the "Myc/Max binding site."

To determine whether experimental induction of c-Myc can lead to the *de novo* activation of telomerase in primary human cells, pre-senescent IMR90 cultures engineered to express the mouse ecotropic receptor (Serrano et al. (1997) Cell 88, 593-602) were transduced with either the pBABE retroviral vector or one encoding a hormone inducible c-Myc-Estrogen Receptor (cMycER) fusion protein (Eilers et al., 1989 Nature 340, 66-68; Littlewood (1995) Nuc. Acids Res. 23, 1686-1690). IMR90 cultures do not possess detectable telomerase activity or TERT gene expression (Nakamura et al., 1997; Meyerson et al., 1997).

Retroviral Infection   The mouse ecotropic receptor was transduced into IMR90 fibroblasts and all subsequent transductions with ecotropic retrovirus were carried out according to Serrano et al. (1997). pBABE-MycER and pBABE vector control viruses were harvested from stable expressing _2 cell lines.

Cell Culture: IMR90 cells were grown in Dulbecco's Modified Eagle Medium (DMEM) (Gibco/BRL) supplemented with 10% fetal bovine serum (FBS), 0.29 mg/mL L-glutamine, 0.03% penicillin and streptomycin, and 25 ug/mL gentamycin sulfate. For the Myc induction studies in IMR90 cells, MycER transduced cells were exposed to 2 uM 4-OHT for 24, 48 and 72 hours. For the promoter studies NIH 3T3 cells were exposed to 1 uM 4-OHT for 24 and 72 hours. In all cases uninduced controls were treated with an equivalent volume of ethanol, the solvent for 4-OHT.

Telomerase Assays: Telomerase activity was measured by a modified telomerase repeat amplification protocol using the TRAPeze telomerase detection kit (Oncor, Gaithersburg, MD) (Kim et al., 1994). Genomic DNA was obtained from vector control or MycER transduced IMR90 fibroblasts. TRAP assays were performed on lysates equivalent to 1000 cells for all samples, with 293T cell lysates serving as a positive control for telomerase activity. PCR internal controls from each experiment were amplified equally. Inactivation of lysate was for 5 minutes at 85 oC prior to the TRAP assay.

In the MycER system, the Myc moiety exists in a latent form bound in a complex with HSP-90 through its ER fusion (Eilers et al., 1989; Littlewood et al., 1995). Upon treatment with 4-hydroxy-tamoxifen (4-OHT), the MycER protein is liberated from HSP-90, resulting in a Myc over-expression phenotype (Eilers et al., 1989; Littlewood et

al., 1995). Employing this cell culture system, 4-OHT treatment of MycER-transduced IMR90 cultures resulted in the marked and sustained activation of telomerase to a level at or above that detected in lysates derived from an equivalent number of telomerase-positive 293T tumor cells, as assayed by the sensitive TRAP assay. In contrast, untreated

5   MycER-transduced or 4-OHT-treated pBABE-transduced IMR90 cultures remained telomerase negative. Western blot analysis confirmed abundant MycER protein levels in the MycER-transduced cultures in the presence or absence of 4-OHT.

Notably, enforced expression of oncogenes such as H-Ras, and cellular modulators of the Rb and p53 pathways (E7, cyclin D1, Mdm2, dominant-negative p53)

10   have not been found to be capable of influencing telomerase activity in IMR90 cells (Wang et al., 1998).

c-Myc Enhancement of hTERT Transcription Requires the Presence of a Cis-Acting Promoter Element: the Proximal Myc-Binding "E-Box"

hTRT Reporter Construction: The pGRN150 (E box deleted), pGRN261

15   (2.5 kbp hTRT reporter) are described above. NIH 3T3 cells were grown in Dulbecco's Modified Eagle Medium (DMEM) (Gibco/BRL) supplemented with 10% fetal bovine serum (FBS), 0.29 mg/mL L-glutamine, 0.03% penicillin and streptomycin, and 25 ug/mL gentamycin sulfate. NIH 3T3 cells were transfected using LipoFectamine reagent (Life Sciences) with 100 ng of a promoter reporter, and 200 ng of pCMX-ß-Galactosidase

20   which served as an internal control for transfection efficiency. Transfected cells were allowed to recover for 6 hours in complete DMEM and then treated with 1 uM 4-OHT or ethanol for 36 hours prior to analysis of secreted alkaline phosphatase activity using the Great EscAPe assay (Clontech). ß -galactosidase activity was assayed by incubation of whole cell extracts with 400 ug/ml ONPG in buffer containing 60 mM Na2HPO4, 40 mM

25   NaH2PO4, 10 mM KCl and 1 mM MgSO4 and relative transfection efficiencies determined by reading absorbance at 415 nm.

Expression of endogenous hTRT following exposure to 4-OHT (or solvent alone) was measured at various times in the presence of 1 _M cyclohexamide in IMR90 fibroblasts transduced with MycER. Reverse transcription of RNA derived from each

30   sample followed by PCR and Southern blotting of the amplified products was carried out as described above. Glyceraldehyde-6-phosphate dehydrogenase (GAPDH) was amplified from the same reverse transcription products as an internal semi-quantitative control and visualized by ethidium bromide staining. Low level expression of hTRT

mRNA was detected in uninduced samples after very long exposures; however, the level of hTRT mRNA did not change over time in the uninduced samples.

The activity of the hTERT promoter was dramatically enhanced by c-Myc-ER in NIH 3T3 cells. The ability of c-Myc-ER to enhance hTERT promoter activity was dependent upon sequences in the hTERT promoter that included an evolutionarily conserved Myc binding site (E-box). To determine whether the increased telomerase activity induced by activation of c-Myc-ER was a result of increased transcription of the hTERT gene we initially examined the effect of 4-OHT induction of c-Myc-ER activity upon hTERT promoter sequences placed upstream of the secreted alkaline phosphatase reporter gene. The hTERT promoter contains two putative Myc-binding sites positioned at -242 and -34 relative to the ATG initiation codon.

NIH 3T3 cells engineered to express c-Myc-ER stably were transfected with constructs containing a secreted alkaline phosphatase reporter under the control of a 2.5 kb fragment of the hTERT promoter, a 2.5 kb fragment of the hTERT promoter lacking the proximal E-box, or a promoterless reporter construct. The basal activity of the wild-type hTERT promoter and that of the hTERT promoter lacking the proximal E-box were equivalent and approximately 3 fold higher than the activity of the promoterless reporter. Induction of c-Myc-ER activity with 1 _M 4-OHT enhanced the activity of the 2.5 kb hTERT promoter approximately 10 fold. By contrast, the activity of the promoter lacking the proximal E-box was not significantly affected by induction of c-Myc-ER. Similarly, the promoterless reporter was not affected by induction of c-Myc-ER. To further confirm the role of the proximal E-box in regulating the hTERT promoter we tested the effect of changing the E-box from CACGTG to CACTCA. The mutation in the E-box reduced the promoter activity due to 4-OHT stimulation to the equivalent of the E-box deletion and 10-fold below the wild-type promoter. This demonstrates that c-Myc-ER is not able to significantly activate an hTERT promoter with an attenuated E-box at -34 and that the E-box at -242 is not able to significantly mediate c-Myc activation. These results suggest that the ability of c-Myc to stimulate the hTERT promoter is mediated via the -34 E-box.

hTERT is a Direct Target of c-Myc Regulated Transcription

To confirm the ability of c-Myc to stimulate transcription of the hTERT gene directly, we assayed for hTERT gene expression in MycER-transduced cultures of IMR90 cells 0, 1, 3 and 9 hours following the addition of 4-OHT. The cultures were

treated with cyclohexamide for 30 minutes prior to addition of 4-OHT to prevent de novo protein synthesis. hTERT expression was undetectable at the zero hour time point for the Myc transduced cultures. Pretreatment of these cells with cyclohexamide alone had no effect on expression of hTERT mRNA. Induction of the c-Myc-ER activity by treatment

5   with 2 M 4-OHT in the presence of 1 cyclohexamide led to a rapid increase in expression of hTERT message.

hTERT expression was detected by 1 hour post-induction, and increased 3 and 9 hours post induction. By contrast, cells treated with solvent alone were not induced to express hTERT. Furthermore, the expression level of GAPDH was similar at all time

10   points in cells treated with 4-OHT or solvent alone. These observations strongly suggest that Myc acts directly upon the hTERT promoter to enhance transcription of the hTERT gene.

Lack of Equivalence of Myc and TERT in Cellular Transformation.

To further explore the functional implications of Myc induction of

15   telomerase activity in primary cells, we examined whether TERT could substitute for c-Myc as an immortalizing agent in the rat embryonic fibroblast (REF) cooperation assay. In this assay, co-transfection of Myc and activated RAS (H-RASG12V) effects the malignant transformation of early passage REFs. This cooperative activity can be quantified by monitoring the number of transformed foci appearing in the monolayer 7 to

20   10 days post-transfection. In two separate experiments, various combinations of the expression constructs encoding c-myc, H-RASG12V, TERT, or vector control were introduced into early passage REFs. Strong cooperative activity was observed in the RAS and Myc co-transfections as evidenced by an average of 34 foci per 10 cm plate; while Ras alone generated between 0 and 3 foci per plate; consistent with previous findings that

25   an immortalizing agent and activated RAS are required for efficient transformation of primary rodent cells (Land et al., 1983). By contrast, co-transfection of TERT and RAS did not generate transformed foci counts above that scored for the RAS alone controls. These results indicate that expression of hTERT is insufficient to account for the immortalizing function of Myc in a rat embryonic fibroblast (REF)

30   cooperation assay.

Effect of c-Myc-ER on the activity of the hTRT promoter in NIH3T3 cells was determined by detection of secreted alkaline phosphatase activity. Cells were treated with 4-OHT for 36 hours. Uninduced cells were treated with solvent alone for 36 hours.

The detected secreted alkaline phosphatase activity was corrected for transfection efficiency in each case using ß -galactosidase.

Example 9: Cloning of mouse TERT promoter

The following example details the cloning of the mouse mTERT promoter.

5 *mTERT Construction* : A hybridization probe (nucleotides 1586-1970) of the mTERT cDNA (pGRN188) was used to identify a recombinant phage (mTERT1) from a 129SV mouse genomic phage library (Stratagene). An 8 kb HindIII fragment of mTERT1 that hybridized to the 1586-1970 probe was subcloned into pBluescript II KS + (Stratagene) to generate clone B2.18. The regions encompassing the initiator and promoter were

10 sequenced. The sequence is provided in Figure 5. The sequence has been deposited as GenBank Accession No. B2.18 AF121949.

The human and mouse promoter sequences were aligned using the GAP program from the Wisconsin GCG package using a value of 48 for gap creation and a value of 3 for gap extension. Using a small portion of the coding region (~ 450 bases) was

15 found to improve the initial alignment. See Figures 4A and 4B.

Conservation of Human and Mouse TERT Promoters

To determine whether the ability of c-Myc to enhance telomerase activity was mediated through increased transcription of the hTERT gene, we compared the sequences of the human and mouse TERT promoters. Alignment of the first 300 bases of

20 the human and mouse promoters indicates a number of conserved regions (Fig. 4A). In particular, the Myc/Max binding site (E-box) located at -34 of the human promoter and at -32 of the mouse promoter, are highly conserved, as discussed above. A second E-box was identified at -242 of the human promoter; however, this site was not conserved in the mouse promoter. These observations raised the possibility that the conserved Myc

25 binding site in particular might play a role in the regulation of hTERT expression by c-Myc

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